

FIG.1A.

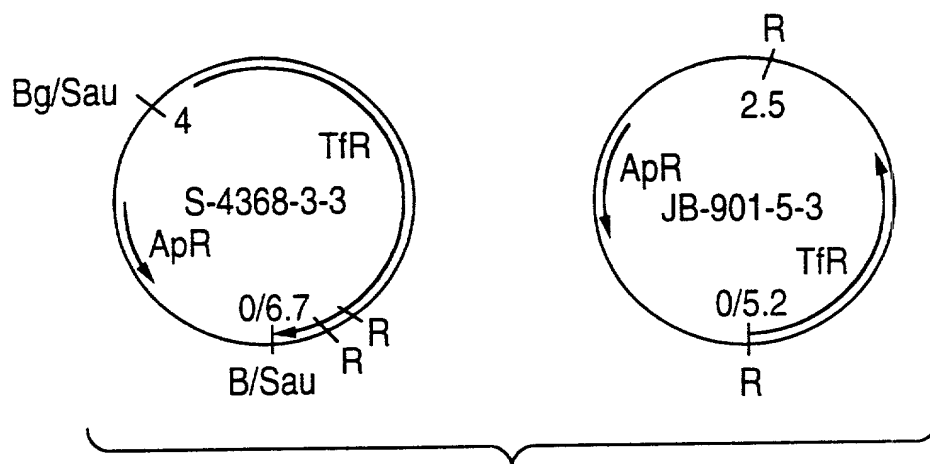


FIG.1B.

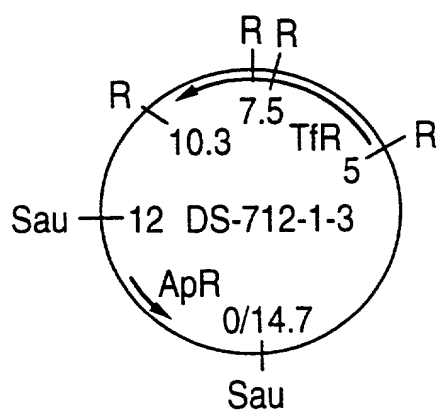


FIG.1C.

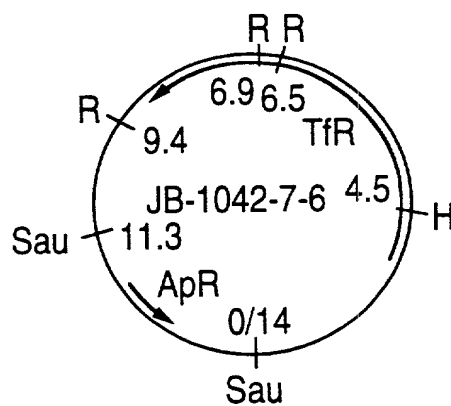
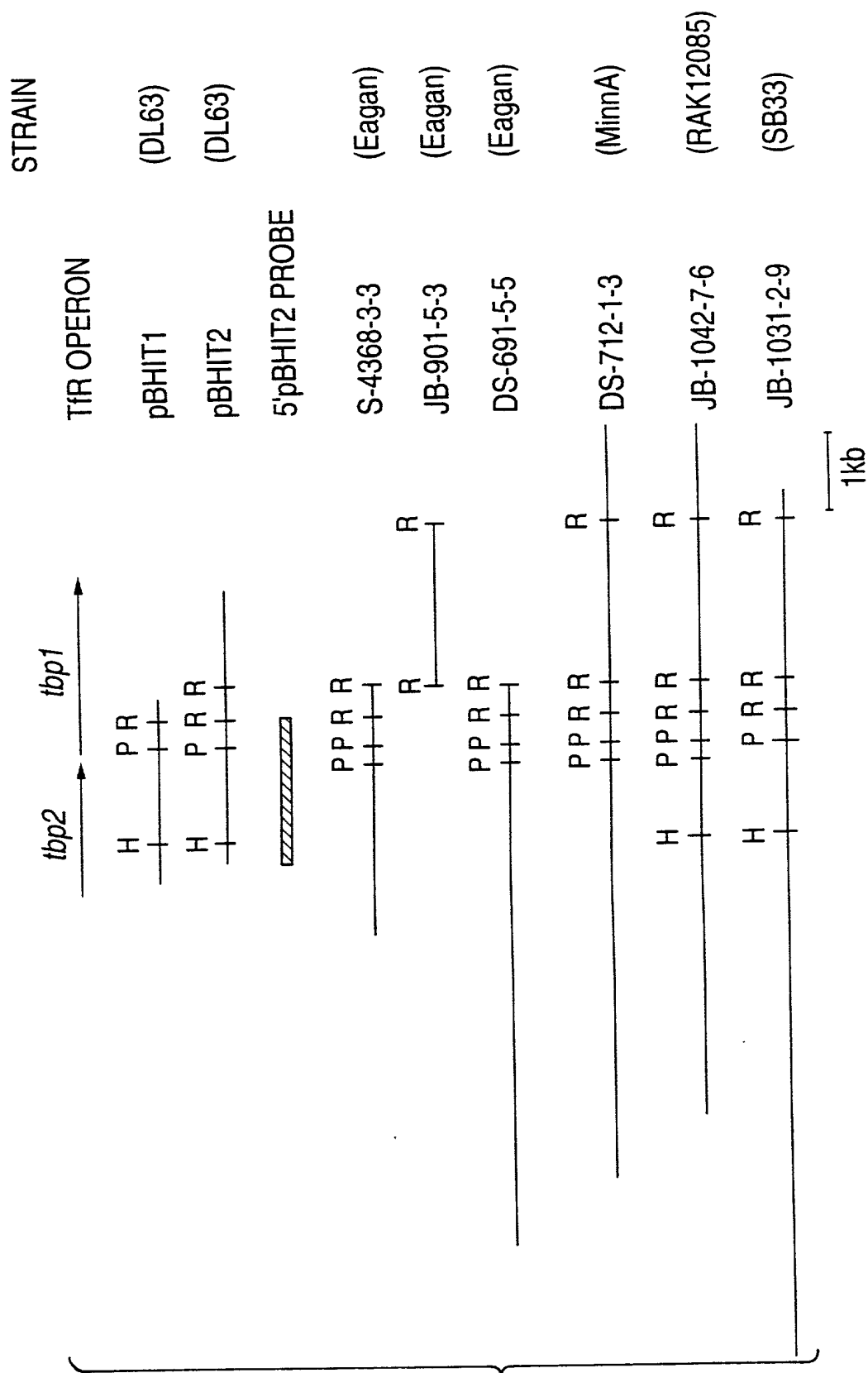


FIG.1D.



**FIG. 2:**

FIG. 3 A.

TATAACTCA ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT

Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe

1

5

10

TTA CTA AGT GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC

Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val

15

20

25

TCT AAT ACC CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT TCA AGT

Ser Asn Thr Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Trp Ser Ser

30

35

40

45

TCA AGA ACA AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA GGG

Ser Arg Thr Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly

50

55

60

GGA GGG ATG AAG TTA GCG GCT CTG AAT CTT TTT GAT AGG A-C AAA CCT

Gly Gly Met Lys Leu Ala Ala Leu Asn Leu Phe Asp Arg Asn Lys Pro

65

70

75

AGT CTC TTA AAT GAA GAT AGC TAT ATG ATA TTT TCC TCA CGT TCT ACG

Ser Leu Leu Asn Glu Asp Ser Tyr Met Ile Phe Ser Ser Arg Ser Thr

80

85

90

# FIG.3B.

ATT GAA GAG GAT GTT AAA AAT GAC AAT CAA AAC GGC GAG CAC CCT ATT  
 Ile Glu Glu Asp Val Lys Asn Asp Asn Gln Asn Gly Glu His Pro Ile  
 95 100 105

GAC TCA ATA GTC GAT OCT AGA GCA CCA AAT TCA AAC GAA AAT CGT CAT  
 Asp Ser Ile Val Asp Pro Arg Ala Pro Asn Ser Asn Glu Asn Arg His  
 110 115 120 125

GGA CAA AAA TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TGG AGT  
 Gly Gln Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser  
 130 135 140

CTA AGA GAT TTA CCA AAT AAA AAG TTT TAT TCA GGT TAC TAT GGA TAT  
 Leu Arg Asp Leu Pro Asn Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr  
 145 150 155

GGC TAT TAC TTT GGC AAT ACA ACT GCC TCT GCA TTA CCT GTA GGT GGC  
 Ala Tyr Tyr Phe Gly Asn Thr Thr Ala Ser Ala Leu Pro Val Gly Gly  
 160 165 170

GTA GCA ACG TAT AAA GGA ACT TGG AGC TTC ATC ACC GCA GCT GAA AAT  
 Val Ala Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn  
 175 180 185

FIG.3C.

GGC AAG AAT TAT GAA TTG TTA AGA AAT TCT GGT GGC GGT CAA GCT TAT  
 Gly Lys Asn Tyr Glu Leu Leu Arg Asn Ser Gly Gly Gln Ala Tyr  
 190 195 200 205  
  
 TCT CGA CGT AGT GCT ACT CCA GAA GAT ATT GAT TTA GAT CGT AAG ACG  
 Ser Arg Arg Ser Ala Thr Pro Glu Asp Ile Asp Leu Asp Arg Lys Thr  
 210 215 220  
  
 GGC TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT  
 Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr  
 225 230 235  
  
 GGA GGA CTT TAT TAT AAT TTA CGT GAA ACA GAT GCT AAT AAA TCA CAA  
 Gly Gly Leu Tyr Tyr Asn Leu Arg Glu Thr Asp Ala Asn Lys Ser Gln  
 240 245 250  
  
 AAT AGA ACA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTT CAT AGC AAC  
 Asn Arg Thr His Lys Leu Tyr Asp Leu Glu Ala Asp Val His Ser Asn  
 255 260 265  
  
 CGA TTC AGG GGT AAA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA  
 Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu  
 270 275 280 285

# FIG. 3D.

CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG CCT  
His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro  
290 295 300

GAG GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT CAC GAA AAA AAA GTT  
Glu Gly Gln Glu Leu Gly Gly Lys Phe Leu Ala His Asp Lys Lys Val  
305 310 315

TTC GGG GTA TTT AGT GCC AAA GAA CAG CAA GAA ACG TCA GAA AAC AAA  
Leu Gly Val Phe Ser Ala Lys Glu Gln Gln Glu Thr Ser Glu Asn Lys  
320 325 330

AAA TTA CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTT AAA  
Lys Leu Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Lys  
335 340 345

ACA ACC AAT GCA ACA GCC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA  
Thr Thr Asn Ala Thr Ala Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr  
350 355 360 365

ACA GCC AGT ACA AAA ACC GAT ACA ACA ACC AAT GCA ACA GCC AAT ACA  
Thr Ala Ser Thr Lys Thr Asp Thr Thr Thr Asn Ala Thr Ala Asn Thr  
370 375 380

FIG.3E.

GAA AAC TTT ACG ACA AAA GAT ATA CCA AGT TTG GGT GAA GCT GAT TAT  
 Glu Asn Phe Thr Lys Asp Ile Pro Ser Leu Gly Glu Ala Asp Tyr  
 385 390 395

CCT TTA ATT GAT AAT TAC CCT GGT CTT TTC CCT GAG AGT GGT GAT  
 Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Ser Gly Asp  
 400 405 410

TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA  
 Phe Ile Ser Ser Lys His Thr Val Gly Lys Lys Thr Tyr Gln Val  
 415 420 425

GAA GCA TGT TGC AGT AAT CTA AGC TAT GTA AAA TTT GGT ATG TAT TAT  
 Glu Ala Cys Cys Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr  
 430 435 440 445

GAA GCC CCA CCT AAA GAA GAA GAA AAA GAA AAA GAA GAC AAA GAC  
 Glu Ala Pro Pro Lys Glu Glu Glu Lys Lys Glu Lys Lys Asp Lys Asp  
 450 455 460

AAA GAA AAA GAA AAA CAA CCG ACA ACA TCT ATC AAG ACT TAT TAT CAA  
 Lys Glu Lys Glu Lys Gln Ala Thr Thr Ser Ile Lys Thr Tyr Tyr Gln  
 465 470 475

CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA ACC GCA AAA GAT TTA  
Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Lys Asp Leu  
560 565 570



# FIG.36.

GCA ATA GAT GGT AAA AAT ACA CAA GGC ACA TCT AAA GTC AAT TTC ACG  
Ala Ile Asp Gly Lys Asn Thr Gln Gly Thr Ser Lys Val Asn Phe Thr  
575 580

GCA ACA GTA AAC GCG GCA TTT TAT GGT CCG CAC GCT ACA GAA TTA GGC  
Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro His Ala Thr Glu Leu Gly  
590 600 605

GGT TAT TTC ACC TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCA TCA  
Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser Ser  
610 615 620

TCC AAT TCA GAA AAG GCA AGA GCT GCC GTT GIG TTT GGA GCT AAA AAA  
Ser Asn Ser Glu Lys Ala Arg Ala Ala Val Phe Gly Ala Lys Lys  
625 630 635

CAA CAA GTA GAA ACA ACC AA GTAATGGAAT ACTAAA A ATG ACT AAA AAA  
Gln Gln Val Glu Thr Thr Lys Met Thr Lys Lys  
640 645

CCC TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT  
Pro Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr  
650 655 660

# FIG.3H.

GTA AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA	
Val Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser	
665	670 675 680
TCT GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC	
Ser Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile	
685	690 695
TCA GTC ACT GCA GAA AAA GTT ACA GAT CGT AAA GAT AAT GAA GTA ACT	
Ser Val Thr Ala Glu Lys Val Arg Asp Arg Lys Asp Asn Glu Val Thr	
700	705 710
CGA CTT GGC AAA ATT ATA AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA	
Gly Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln	
715	720 725
GTA TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA GGG ATT TCA GTT	
Val Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val	
730	735 740
GTA GAA CAA GGT CGC GGT GCA AGT TCT CGA TAT TCT ATT CGT GGT ATG	
Val Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met	
745	750 755 760

FIG.31.

GAC AGA AAT AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA	
Asp Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln	765 770 775
TCT TAT GTA GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC	
Ser Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly	780 785 790
ACT GGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA	
Thr Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu	795 800 805
ATA AGC AAG GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT	
Ile Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala	810 815 820
GGT TCT GTA ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA	
Gly Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly	825 830 835 840
GAC AAA TCA TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT	
Asp Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn	845 850 855

## FIG.3J.

AAA GGC TTT ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT  
 Lys Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe  
 860 865 870  
  
 GAA GGG GTC GCC ATT TAC ACT CAC CGA AAT TCA ATT GAA ACC CAA GTC  
 Glu Gly Val Ala Ile Tyr Thr His Arg Asn Ser Ile Glu Thr Gln Val  
 875 880 885  
  
 CAT AAA GAT GCA TTA AAA GGC GTG CAA AGT TAT GAT CGA TTC ATC GCC  
 His Lys Asp Ala Leu Lys Lys Gly Val Gln Ser Tyr Asp Arg Phe Ile Ala  
 890 895 900  
  
 ACA ACA GAG GAT CAA TCT GCA TAC TTT GTG ATG CAA GAT GAG TGT CTA  
 Thr Thr Glu Asp Gln Ser Ala Tyr Phe Val Met Gln Asp Glu Cys Leu  
 905 910 915 920  
  
 GAT GGT TAT GAC AAG TGT AAA ACT TCA CCC AAA CGA CCT GCG ACT TTA  
 Asp Gly Tyr Asp Lys Cys Lys Thr Ser Pro Lys Arg Pro Ala Thr Leu  
 925 930 935  
  
 TCC ACC CAA AGA GAA ACC GTA AGC GTT TCA GAT TAT ACG GGG GCT AAC  
 Ser Thr Gln Arg Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn  
 940 945 950

# FIG.3K.

CGT ATC AAA CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA  
 Arg Ile Lys Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu  
 955 960 965

AGA GCA GGT TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT  
 Arg Gly Gly Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe  
 970 975 980

GAA TTC ACA CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT  
 Glu Phe Thr Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala  
 985 990 995 1000

TAT TTA AGG CCA ACA GAA GAC AAG GAT TTA CAA AGT CGC CCT TTT TAT  
 Tyr Leu Arg Pro Thr Glu Asp Lys Asp Leu Gln Ser Arg Pro Phe Tyr  
 1005 1010 1015

CCA AAG CAA GAT TAT GGT GCA TAT CAA CAT ATT GGT GAT GGC AGA GGC  
 Pro Lys Gln Asp Tyr Gly Ala Tyr Gln His Ile Gly Asp Gly Arg Gly  
 1020 1025 1030

GTT AAA TAT GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG  
 Val Lys Tyr Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln  
 1035 1040 1045

# FIG.3L.

CGT GTA GGT ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC	
Arg Val Gly Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile	
1050	1055
ATT GAC AAA GCG GTG TTA AGT GCT AAT CAA ACA TCA TAC TTG ACA	
Ile Asp Lys Ala Val Leu Ser Ala Asn Gln Thr Ser Tyr Leu Thr	
1065	1070
	1075
	1080
GTT ATA TGC GAC ATA CGC ATT GCA GTC TTT ATC CAT AAT CCA AGT AAG	
Val Ile Cys Asp Ile Arg Ile Ala Val Phe Ile His Asn Pro Ser Lys	
1085	1090
	1095
AAT TGC CGC CCA ACA CTT GAT AAA CCT TAT TCA TAC TAT CAT TCT GAT	
Asn Cys Arg Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr His Ser Asp	
1100	1105
	1110
AGA AAT GTT TAT AAA GAA AAA CAT AAC ATG TTG CAA TTG AAT TTA GAG	
Arg Asn Val Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu	
1115	1120
	1125
AAA AAA ATT CAA CAA AAT TGG CTT ACT CAT CAA ATT GCC TTC AAT CTT	
Lys Lys Ile Gln Asn Trp Leu Thr His Gln Ile Ala Phe Asn Leu	
1130	1135
	1140

# FIG. 3M.

GGT TTT GAT GAC TTT ACT TCC GCA CTT CAG CAT AAA GAT TAT TTA ACT  
Gly Phe Asp Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr  
1145 1150 1155 1160

CGA CGT GTT ATC GCT ACG GCA AGT AGT ATT TCA GAG AAA CGT GGT GAA  
Arg Arg Val Ile Ala Thr Ala Ser Ser Ile Ser Glu Lys Arg Gly Glu  
1165 1170 1175

GCA AGA AGA AAT GGT TTA CAA TCA AGT CCT TAC TTA TAC CCA ACA CCA  
Ala Arg Arg Asn Gly Leu Gln Ser Ser Pro Tyr Leu Tyr Pro Thr Pro  
1180 1185 1190

AAA GCA GAG TTG GTA GGA GCA GAT CTT TGT AAT TAT CAA GGT AAG TCC  
Lys Ala Glu Leu Val Gly Gly Asp Leu Cys Asn Tyr Gln Gly Lys Ser  
1195 1200 1205

TCT AAT TAC AGT GAC TGT AAA GTG CCG TTA ATT AAA GGG AAA AAT TAT  
Ser Asn Tyr Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr  
1210 1215 1220

TAT TTC GCA GCA CGC AAT AAT ATG GCA TTA GCG AAA TAC GTT GAT TTA  
Tyr Phe Ala Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu  
1225 1230 1235 1240

## FIG.3N.

GGT TTA GGT ATG AGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA  
Gly Leu Gly Met Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser  
1245 1250 1255

ACT ATT AGT GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT  
Thr Ile Ser Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile  
1260 1265 1270

GTC ATA AAA CCA ACG GAA TGG CTT GAT CTT TCT TAT CGC CTT TCT ACT  
Val Ile Lys Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr  
1275 1280 1285

CGA TTT AGA AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CGG TAT GGT  
Gly Phe Arg Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly  
1290 1295 1300

GGC AAG GAT ACC GAT GTT TAT ATA GGT AAA TTT AAG CCT GAA ACA TCT  
Gly Lys Asp Thr Asp Val Tyr Ile Gly Lys Phe Lys Pro Glu Thr Ser  
1305 1310 1315 1320

CGT AAC CAA GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT  
Arg Asn Gln Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile  
1325 1330 1335



**FIG.30.**

GAG ATC AGT CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT  
 Glu Ile Ser His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala  
 1340 1345 1350

GAA GAA CTT AGT AAA AAT CGA ACT ACT CGA AAG GGC AAT TAT CGA TAT  
 Glu Glu Leu Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr  
 1355 1360 1365

CAT AAT GCA CAA AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA  
 His Asn Ala Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln  
 1370 1375 1380

TTA GAT TTT AAT GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA  
 Leu Asp Phe Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala  
 1385 1390 1395 1400

ACA TTT GCT TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT  
 Thr Phe Ala Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala  
 1405 1410 1415

GGT TTA GCT TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC  
 Gly Leu Ala Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser  
 1420 1425 1430

## FIG. 3P.

CGT TAT ATC ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA  
Arg Tyr Ile Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly  
1435 1440 1445

ATT AAG ACA ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG  
Ile Lys Thr Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu  
1450 1455 1460

CTA GGA AAA CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA  
Leu Gly Lys Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr  
1465 1470 1475 1480

AGA AAA CTT ACT CGG GCA TGG CAT ATC TTA GAT GTA TCG CGT TAT TAC  
Arg Lys Leu Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr  
1485 1490 1495

ATG GTG AAT AGA AGT ATT TTG TTC CGA TTA GGA GTA TAT AAT TTA TTA  
Met Val Asn Arg Ser Ile Leu Phe Arg Leu Gly Val Tyr Asn Leu Leu  
1500 1505 1510

AAC TAT CGC TAT GTC ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA GGT  
Asn Tyr Arg Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly  
1515 1520 1525

## FIG.3Q.

GCG GTC AAT CAA CAT CAA AAT GTT GGT AAC TAT ACT CGC TAC GCA GCA	
Ala Val Asn Gln His Gln Asn Val Gly Asn Tyr Thr Arg Tyr Ala Ala	
1530	1535
	1540
TCA GGA CGA AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAA	
Ser Gly Arg Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe	
1545	1550
	1555

# FIG. 4 A.

GCCCAAGCTA CATTGGTTAA TGATAAGCCT ATAAATGATA AGAAAGAAAT TTGTTTTACG

CCATTTTTCA TATTTTATCC ATGAACTTAA AAAACTCTAA CTTGACATTAA TTACAAAAAA

AGATCAATAA TGCGAATTAT TATCAATTTT <sup>RGS</sup>GTATGAGTAT ATAATTC TATG AAA TCT  
Met Lys Ser  
1

GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT GCT TGT AGC  
Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Ser Ala Cys Ser  
5 10 15

GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC CCC TCT TCT  
Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr Pro Ser Ser  
20 25 30 35

AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA AAA TCT AAT  
Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys Lys Ser Asn  
40 45 50

TTG AAA AAG TTG TTC ATT CCT TCT TTA GGA GGA GGG ATG AAA TTG GTG  
Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Met Lys Leu Val  
55 60 65

**FIG.4B.**

GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA AAT GAA GAT	
Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu Asn Glu Asp	
	70                      75                      80
GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA AAG GAT GTT	
Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu Lys Asp Val	
	85                      90                      95
AAA GAT AAC AAT AAA AAC GCG GCG GAC CTT ATT GGC TCA ATA GAC GAG	
Lys Asp Asn Asn Lys Lys Asn Gly Ala Asp Leu Ile Gly Ser Ile Asp Glu	
100                      105                      110                      115	
CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GGA CAA AAA TAT GTA	
Pro Ser Thr Thr Asn Pro Pro Glu Lys His Gly Gln Lys Tyr Val	
	120                      125                      130
TAT TCA GCG CTT TAT TAT ACT CCA TCG TGG AGT TTA AAC GAT TCT AAA	
Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Ser Trp Ser Leu Asn Asp Ser Lys	
	135                      140                      145
AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT TAT CGT AAT	
Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn	
	150                      155                      160

# FIG.4C.

AAA ACT GCA ACA AAC TTG CCA GTA AAC GGT GTA GCT AAA TAC AAA GGA  
Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys Tyr Lys Gly  
165 170 175

ACT TGG GAT TTC ATC ACT ACT GCA ACT AAA AAT GGC AAA CGT TAT CCT TTG  
Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg Tyr Pro Leu  
180 185 190 195

TTA AGT AAT GGC AGT CAC GCT TAT TAT CCA CGT AGT GCA ATT CCA GAA  
Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala Ile Pro Glu  
200 205 210

GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA GGC TTA ATA  
Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile Gly Leu Ile  
215 220 225

AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA GGA CAA CTG  
Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr Gly Gln Leu  
230 235 240

TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA AAG AAA AAA  
Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu Lys Lys Lys  
245 250 255

# FIG.4D.

CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC AGG GGT ACA  
 Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe Arg Gly Thr 275  
 260 265 270

GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT ACC AGC GAG  
 Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe Thr Ser Glu 290  
 280 285

CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG  
 Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly 305  
 295 300

GGG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GGG GTA TTT AGT GCC  
 Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val Phe Ser Ala 320  
 310 315

AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TCC AAG GAA ACC TTA  
 Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys Glu Thr Leu 335  
 325 330

ATT GAT GGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC GAT GCA AAA  
 Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr Asp Ala Lys 355  
 340 345 350

# FIG.4E.

ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC GAT ACA ACC  
 Thr Asn Ala Thr Thr Ser Thr Ala Ala Asn Thr Thr Thr Asp Thr Thr  
 360 365 370

GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA GAT ATA TCA  
 Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu Asp Ile Ser  
 375 380 385

AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT CCT ATT CCA  
 Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys Tyr Pro Ile Pro  
 390 395 400

CIT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT AAG CAT CAT  
 Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser Lys His His  
 405 410 415

ACT GTA GGA AAT AAA CCG TAT AAA GTG GAA GCA TGT TGC AGT AAT CTA  
 Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys Ser Asn Leu  
 420 425 430 435

AGC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT AAA GAA AAA  
 Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu Lys Glu Lys  
 440 445 450



## FIG.4F.

GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA AAA GAA AAA  
 Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu Lys Glu Lys  
 455 460 465

GAA AAA GAC AAA GAC AAA GAA AAA CAA ACG GCG GCA ACG ACC AAC ACT  
 Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr Thr Asn Thr  
 470 475 480

TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC GAC ATA CCT  
 Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp Asp Ile Pro  
 485 490 495

AAA ACA CGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT TAT ATT ACT  
 Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly Tyr Ile Thr  
 500 505 510 515

GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA CGC GAT AAA  
 Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Asp Lys  
 520 525 530

AAT GCT GTC GCC GAG TTT AAT GAT TTT GCC GAG AAA AAG CTA ACA  
 Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys Lys Leu Thr  
 535 540 545

# FIG.4G.

GGC GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTA TTT AGT ATT GAG  
Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe Ser Ile Glu  
550 555 560

GCA AAC TTT AAT AAT AGT AGT AAT GCC TTC ACT GGT ACA GCA ACC GCA  
Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr Ala Thr Ala  
565 570 575

ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA AAT ACC CCA  
Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys Asn Thr Pro  
580 585 590 595

ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT  
Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala  
600 605 610

TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT ACA GCT ACA  
Ser Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Asn Ser Thr Ala Thr  
615 620 625

AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCC AAT TCA AAA AAT  
Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Asn Ser Lys Asn  
630 635 640

FIG.4H.

GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA GAA ACA ACC  
 Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val Glu Thr Thr  
 645 650 655

AAA TAATGGAATA CTAAAA ATG ACT AAA AAA CCC TAT TTT CGC CTA AGT  
 Lys Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser  
 660 665 670

ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA  
 Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln  
 675 680 685

AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA  
 Ser Ile Lys Asp Thr Lys Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln  
 690 695 700

AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA  
 Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys  
 705 710 715

ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GGA CTT GGC AAA ATT ATC  
 Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Ile  
 720 725 730

**FIG.41.**

AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT ATT CGT GAT	
Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp	750
735	740 745
CTA ACA CGC TAT GAT CCA GCG ATT TCA GTT GTA GAA CAA GGT CGC GGT	
Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly	765
755	760
GCA AGT TCT CGA TAT TCT ATT CGT GGT ATG GAC AGA AAT AGA GTT GCT	
Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala	780
770	775
TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA AGC	
Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser	795
785	790
CCT TTA GTT GCT CGT TCA GGA TAT TCT GCG ACT GGT GCA ATT AAT GAA	
Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala Ile Asn Glu	810
800	805
ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG GCG GCG AGT	
Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser	830
815	820 825

# FIG.4J.

TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA ACA TTT CAA  
 Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln  
 835 840 845

AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG GGA ATT  
 Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile  
 850 855 860

CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT  
 Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser  
 865 870 875

TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA GGG CTA GCC ATT TAC  
 Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu Gly Leu Ala Ile Tyr  
 880 885 890

ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA  
 Thr Gln Arg Asn Ser Ile Glu Thr Thr Gln Val His Lys Asp Ala Leu Lys  
 895 900 905 910

GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT AAA TCT TCA  
 Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp Lys Ser Ser  
 915 920 925

# FIG.4K.

GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT GGT GAT GAC AAG TGT  
Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp Asp Lys Cys  
930 935 940

GCA GGC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA ACC GTA AGC  
Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu Thr Val Ser  
945 950 955

GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA OCT AAT CCA ATG AAA  
Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met Lys  
960 965 970

TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GCG TAT CAT TTT TCT GAA  
Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His Phe Ser Glu  
975 980 985 990

CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA CAA AAA TTT GAT  
Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe Asp  
995 1000 1005

ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA GAA AGA CCG  
Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr Glu Arg Arg  
1010 1015 1020

# FIG.4L.

GAT GAT AGT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT CGT GCA TAT  
 Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His Gly Ala Tyr  
 1025 1030 1035  
  
 CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT GCA AGT GGG CTT TAT  
 Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser Gly Leu Tyr  
 1040 1045 1050  
  
 TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA CGT ATT GAA TAT ATT TAC  
 Phe Asp Glu His His Arg Lys Lys Gln Arg Val Gly Ile Glu Tyr Ile Tyr  
 1055 1060 1065 1070  
  
 GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GTG TTA AGT GCT  
 Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser Ala  
 1075 1080 1085  
  
 AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CGA CAT ACG CAT TGC  
 Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His Thr His Cys  
 1090 1095 1100  
  
 AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CTT GAT AAA  
 Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Leu Asp Lys  
 1105 1110 1115

# FIG.4M.

CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT TAT AAA GAA AAA CAT	
Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys Glu Lys His	
1120	1125 1130
AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA AAT TGG CTT	
Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp Leu	
1135	1140 1145 1150
ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA GCG	
Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser Ala	
1155	1160 1165
CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT ACG GCA GAT	
Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala Thr Ala Asp	
1170	1175 1180
AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA AAT GGT TTG	
Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg Asn Gly Leu	
1185	1190 1195
CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT TTT GCA GCA	
Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr Phe Ala Gly	
1200	1205 1210



## FIG. 4N.

CAA GAT CAT TGT AAT TAT CAA GGT AGC TCC TCT AAT TAC AGA GAC TGT  
 Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Asn Tyr Arg Asp Cys  
 1215 1220 1225 1230  
  
 AAA GTG CGG TTA ATT AAA GGG AAA AAT TAT TTC GCA GCA CGC AAT  
 Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn  
 1235 1240 1245  
  
 AAT ATG GCA TTA GGG AAA TAC GTT GAT TTA GGT TTA GGT ATT CGG TAT  
 Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr  
 1250 1255 1260  
  
 GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT GGT AAA  
 Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys  
 1265 1270 1275  
  
 TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA  
 Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys Pro Thr Glu  
 1280 1285 1290  
  
 TGG CTT GAT CTT TCT TAT CGC CTT TCT ACT GGA TTT AGA AAT CCT AGT  
 Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser  
 1295 1300 1305 1310

## FIG.40.

TTT TCT GAA ATG TAT GGT TGG CGG TAT GGT GCG AAG AAT GAC GAG GTT  
 Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn Asp Glu Val  
 1315 1320 1325  
  
 TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT  
 Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly  
 1330 1335 1340  
  
 CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT  
 Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser  
 1345 1350 1355  
  
 AAT GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AGT AAA AAT  
 Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Ser Lys Asn  
 1360 1365 1370  
  
 GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA  
 Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys  
 1375 1380 1385 1390  
  
 TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT GGT TTA TGG  
 Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp  
 1395 1400 1405

## FIG.4P.

AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CAA GTA  
Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Gln Val  
1410 1415 1420

AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC GTA AGC AGT  
Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser  
1425 1430 1435

TAT TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GGC  
Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly  
1440 1445 1450

TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA  
Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln  
1455 1460 1465 1470

TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT GCA TTA GGT  
Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly  
1475 1480 1485

AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG  
Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp  
1490 1495 1500

## FIG. 4Q.

CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA AAT ATT ATG  
His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met  
1505 1510 1515

CIT CGA TTA GCG ATA TAT AAT TTA TTC AAC TAT CGC TAT GTT ACT TGG  
Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp  
1520 1525 1530

GAA GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT  
Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn  
1535 1540 1545 1550

GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA AAC TAT ACC TTA  
Val Gly Ser Tyr Thr Arg Tyr Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu  
1555 1560 1565

ACA TTA GAA ATG AAA TTC TAAATTAAAA TGCGCCAGAT GGACTAGATA  
Thr Leu Glu Met Lys Phe  
1570

TGCTATATCT ATACCTTACT GCGGCATCCT TTTCTGTCT ATAATCTGCT TAAGTGA AAA

ACCAAACCTG GATTTTAC AAGATCTTT CACACATTTA TTG

FIG. 5 A.

ATTGTTGTTTA CGCCATTITTT CATATTTTAT CCATGAACCT AAAAAACICT AACTTGACAT<sup>-35</sup>  
 TATTACAAAA AAAGATCAAT AATGCGAATT ATTATCAATT TTGTATGAGT ATATAATTCT<sup>-10'</sup>  
 ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT<sup>ROS</sup>  
 Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser  
 1 5 10 15  
 GCT TGT AGC GGA GGG GGT TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC  
 Ala Cys Ser Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr  
 20 25 30  
 CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA AAA  
 Pro Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Lys  
 35 40 45  
 AAA TCT AAT TTG AAA AAG TTG TTC ATT CCT TCT TTA GGA GGA GGG ATG  
 Lys Ser Asn Leu Lys Lys Leu Phe Ile Pro Ser Leu Gly Gly Met  
 50 55 60  
 AAA TTG GTG GCT CAG AAT CTT CGT GGT AAT AAA GAA CCT AGT TTC TTA  
 Lys Leu Val Ala Gln Asn Leu Arg Gly Asn Lys Glu Pro Ser Phe Leu  
 65 70 75 80

**FIG.5B.**

AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ACG ATT GAA	
Asn Glu Asp Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Thr Ile Glu	95
	85
	90
AAG GAT GTT AAA GAT AAC AAT AAA AAC GGG GCG GAC CTT ATT GGC TCA	
Lys Asp Val Lys Asp Asn Asn Lys Asn Gly Ala Asp Leu Ile Gly Ser	110
	100
	105
ATA GAC GAG CCT AGT ACA ACA AAT CCA CCC GAA AAG CAT CAT GGA CAA	
Ile Asp Glu Pro Ser Thr Thr Asn Pro Pro Glu Lys His His Gly Gln	125
	115
	120
AAA TAT GTA TAT TCA GGG CTT TAT TAT ACT CCA TCG TGG AGT TTA AAC	
Lys Tyr Val Tyr Ser Gly Leu Tyr Tyr Thr Pro Ser Trp Ser Leu Asn	140
	130
	135
GAT TCT AAA AAC AAG TTT TAT TTA GGT TAC TAT GGA TAT GCG TTT TAT	
Asp Ser Lys Lys Asn Lys Phe Tyr Leu Gly Tyr Tyr Gly Tyr Ala Phe Tyr	160
	145
	150
	155
TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AAC GGT GTA GCT AAA	
Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Asn Gly Val Ala Lys	175
	165
	170

# FIG. 5C.

TAC AAA GGA ACT TGG GAT TTC ATC ACT GCA ACT AAA AAT GGC AAA CGT  
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys Asn Gly Lys Arg  
180 185 190

TAT CCT TTG TTA AGT AAT GGC AGT CAC GCT TAT TAT CGA CGT AGT GCA  
Tyr Pro Leu Leu Ser Asn Gly Ser His Ala Tyr Tyr Arg Arg Ser Ala  
195 200 205

ATT CCA GAA GAT ATT GAT TTA GAA AAT GAT TCA AAG AAT GGT GAT ATA  
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Ser Lys Asn Gly Asp Ile  
210 215 220

GGC TTA ATA AGT GAA TTT AGT GCA GAT TTT GGG ACT AAA AAA CTG ACA  
Gly Leu Ile Ser Glu Phe Ser Ala Asp Phe Gly Thr Lys Lys Leu Thr  
225 230 235 240

GGA CAA CTG TCT TAC ACC AAA AGA AAA ACT AAT AAT CAA CCA TAT GAA  
Gly Gln Leu Ser Tyr Thr Lys Arg Lys Thr Asn Asn Gln Pro Tyr Glu  
245 250 255

AAG AAA AAA CTC TAT GAT ATA GAT GCC GAT ATT TAT AGT AAT AGA TTC  
Lys Lys Lys Leu Tyr Asp Ile Asp Ala Asp Ile Tyr Ser Asn Arg Phe  
260 265 270

FIG. 5D.

AGG GGT ACA GTA AAG CCA ACC GAA AAA GAT TCT GAA GAA CAT CCC TTT  
 Arg Gly Thr Val Lys Pro Thr Glu Lys Asp Ser Glu Glu His Pro Phe  
 275 280 285  
 ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAT GCG CCT AAT GCT GAA  
 Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu  
 290 295 300  
 GAA CTA GCG GCG AAA TTT TTA GCT ACG GAT AAC CGA GTT TTT GCG GTA  
 Glu Leu Gly Gly Lys Phe Leu Ala Thr Asp Asn Arg Val Phe Gly Val  
 305 310 315 320  
 TTT AGT GCC AAA GAA ACG GAA GAA ACA AAA AAG GAA GCG TTA TOC AAG  
 Phe Ser Ala Lys Glu Thr Glu Glu Thr Lys Lys Glu Ala Leu Ser Lys  
 325 330 335  
 GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT TTC TCT ACT AAA AAA ACC  
 Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr Phe Ser Thr Lys Lys Thr  
 340 345 350  
 GAT GCA AAA ACC AAT GCA ACA ACC AGT ACC GCA GCT AAT ACA ACA ACC  
 Asp Ala Lys Thr Asn Ala Thr Ser Thr Ala Ala Asn Thr Thr Thr  
 355 360 365



FIG.5E.

GAT ACA ACC GCC AAT ACA ATA ACC GAT GAA AAA AAC TTT AAG ACG GAA  
 Asp Thr Thr Ala Asn Thr Ile Thr Asp Glu Lys Asn Phe Lys Thr Glu  
 370 375 380

GAT ATA TCA AGT TTT GGT GAA GCT GAT TAT CTG TTA ATT GAC AAA TAT  
 Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Lys Tyr  
 385 390 395 400

CCT ATT CCA CTT TTA CCT GAT AAA AAT ACT AAT GAT TTC ATA AGT AGT  
 Pro Ile Pro Leu Leu Pro Asp Lys Asn Thr Asn Asp Phe Ile Ser Ser  
 405 410 415

AAG CAT CAT ACT GTA GGA AAT AAA CGC TAT AAA GTG GAA GCA TGT TGC  
 Lys His His Thr Val Gly Asn Lys Arg Tyr Lys Val Glu Ala Cys Cys  
 420 425 430

AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT GAA GAC CCA CTT  
 Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Pro Leu  
 435 440 445

AAA GAA AAA GAA ACA GAA ACA GAA ACA GAA ACA GAA AAA GAC AAA GAA  
 Lys Glu Lys Glu Thr Glu Thr Glu Thr Glu Thr Glu Lys Asp Lys Glu  
 450 455 460

**FIG.5F.**

AAA GAA AAA GAA GAC AAA GAC AAA GAA AAA CAA ACG GCG GCA ACG	
Lys Glu Lys Glu Lys Asp Lys Asp Lys Glu Lys Gln Thr Ala Ala Thr	
465	470 475 480
ACC AAC ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT CCC AAG GAC	
Thr Asn Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Pro Lys Asp	
485	490 495
GAC ATA CCT AAA ACA GGA AGT GCA AAA TAT CAT GGT AGT TGG TTT GGT	
Asp Ile Pro Lys Thr Gly Ser Ala Lys Tyr His Gly Ser Trp Phe Gly	
500	505 510
TAT ATT ACT GAC GGT AAG ACA TCT TAC TCC CCC AGT GGT GAT AAG AAA	
Tyr Ile Thr Asp Gly Lys Thr Ser Tyr Ser Pro Ser Gly Asp Lys Lys	
515	520 525
CGC GAT AAA AAT GCT GTC GCC GAG TTT AAT GTT GAT TTT GCC GAG AAA	
Arg Asp Lys Asn Ala Val Ala Glu Phe Asn Val Asp Phe Ala Glu Lys	
530	535 540
AAG CTA ACA GGC GAA TTA AAA CGA CAC GAT ACT GGA AAT CCC GTA TTT	
Lys Leu Thr Gly Glu Leu Lys Arg His Asp Thr Gly Asn Pro Val Phe	
545	550 555 560

# FIG.56.

AGT ATT GAG GCA AAC TTT AAT AAT AGT AGT AAT GCC TTC ACT GGT ACA  
 Ser Ile Glu Ala Asn Phe Asn Asn Ser Ser Asn Ala Phe Thr Gly Thr  
 565 570 575

GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAA AAT AGT CAA AAT AAA  
 Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Lys Asn Ser Gln Asn Lys  
 580 585 590

AAT ACC CCA ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT GGA  
 Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr Gly  
 595 600 605

CCT AAG GCT TCT GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAT TCT  
 Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Ser  
 610 615 620

ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA TCT TCA TCA TCC AAT  
 Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Ser Ser Ser Ser Asn  
 625 630 635 640

TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT GCG AGA CAA CAA GTA  
 Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly Ala Arg Gln Gln Val  
 645 650 655

# FIG.5H.

GAA ACA ACC AAA TAATGGAATA CTAAAA ATG ACT AAA AAA CCC TAT TTT	
Glu Thr Thr Lys	Met Thr Lys Lys Pro Tyr Phe
660	665
CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA	
Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala	
670	680
GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG	
Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser Glu Val	
685	695
GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT	
Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser Val Thr	
700	715
GCA GAA AAA ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT CGA CTT CGC	
Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly Leu Gly	
720	730
AAA ATT ATC AAA ACT AGT GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT	
Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val Leu Asn	
735	745

# FIG. 51.

ATT CGT GAT CTA ACA CGC TAT GAT CCA GGG ATT TCA GTT GTA GAA CAA	
Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu Gln	750 760
GGT CGC GGT GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG GAC AGA AAT	
Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn	765 770 775
AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA	
Arg Val Ala Leu Leu Val Val Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val	780 785 790 795
GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC ACT GGT GCA	
Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr Gly Ala	800 805 810
ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG	
Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile Ser Lys	815 820 825
CGG GGG AGT TCT TCT GAG TAT GGT AAT GGA CCA CTA CCT GGT TCT GTA	
Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val	830 835 840

**FIG.5J.**

ACA TTT CAA AGC AAA TCA GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA  
 Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser  
 845 850 855

TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT  
 Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe  
 860 865 870 875

ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA GGG CTA  
 Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Phe Glu Gly Leu  
 880 885 890

GCC ATT TAC ACT CAA CGA AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT  
 Ala Ile Tyr Thr Gln Arg Asn Ser Ile Glu Thr Gln Val His Lys Asp  
 895 900 905

GCA TTA AAA GGC GTA CAA AGT TAT GAT CGA TTA ATC GCC ACA ACA GAT  
 Ala Leu Lys Gly Val Gln Ser Tyr Asp Arg Leu Ile Ala Thr Thr Asp  
 910 915 920

AAA TCT TCA GGA TAC TTT GIG ATA CAA GGT GAG TGT CCA AAT GGT GAT  
 Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn Gly Asp  
 925 930 935

## FIG.5K.

GAC AAG TGT GCA GCC AAG CCA CCT GCG ACT TTA TCC ACC CAA AGC GAA  
 Asp Lys Cys Ala Ala Lys Pro Pro Ala Thr Leu Ser Thr Gln Ser Glu  
 940 945 950 955  
  
 ACC GTA AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA CCT AAT  
 Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn  
 960 965 970  
  
 CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GCG TAT CAT  
 Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly Tyr His  
 975 980 985  
  
 TTT TCT GAA CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA CAA  
 Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln  
 990 995 1000  
  
 AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGC CCA ACA  
 Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Ser Pro Thr  
 1005 1010 1015  
  
 GAA AGA CCG GAT GAT AGT AGT CGT TCT TTT TAT CCA ATG CAA GAT CAT  
 Glu Arg Arg Asp Asp Ser Ser Arg Ser Phe Tyr Pro Met Gln Asp His  
 1020 1025 1030 1035

# FIG. 5L.

GGT GCA TAT CAA CAT ATT GAG GAT GGC AGA GGC GTT AAA TAT GCA AGT  
Gly Ala Tyr Gln His Ile Glu Asp Gly Arg Gly Val Lys Tyr Ala Ser  
1040 1045 1050

GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA CGT ATT GAA  
Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu  
1055 1060 1065

TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GTG  
Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val  
1070 1075 1080

TTA AGT GCT AAT CAA CAA AAC AAC ATC ATA CTT GAC AGT TAT ATG CGA CAT  
Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Arg His  
1085 1090 1095

ACG CAT TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA  
Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr  
1100 1105 1110 1115

CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT TAT AAA  
Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val Tyr Lys  
1120 1125 1130



# FIG. 5M.

GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA AAT CAA CAA  
 Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln  
 1135 1140 1145

AAT TGG CTT ACT CAT CAA AAT GTC TTC AAT CTT GGT TTT GAT GAC TTT  
 Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe  
 1150 1155 1160

ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ATC GCT  
 Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Ile Ala  
 1165 1170 1175

ACG GCA GAT AGT ATT CCA AGG AAA CCT GGT GAA ACT GGT AAA CCA AGA  
 Thr Ala Asp Ser Ile Pro Arg Lys Pro Gly Glu Thr Gly Lys Pro Arg  
 1180 1185 1190 1195

AAT GGT TTG CAA TCA CAA CCT TAC TTA TAC CCA AAA CCA GAG CCA TAT  
 Asn Gly Leu Gln Ser Gln Pro Tyr Leu Tyr Pro Lys Pro Glu Pro Tyr  
 1200 1205 1210

TTT GCA GCA CAA GAT CAT TGT AAT TAT CAA GGT AGC TCC TCT AAT TAC  
 Phe Ala Gly Gln Asp His Cys Asn Tyr Gln Gly Ser Ser Ser Asn Tyr  
 1215 1220 1225

## FIG.5N.

AGA GAC TGT AAA GTG CCG TTA ATT AAA GGG AAA AAT TAT TAT TTC GCA  
Arg Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala  
1230 1235 1240

GCA CGC AAT AAT ATG GCA TTA GGG AAA TAC GTT GAT TTA GGT TTA GGT  
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly  
1245 1250 1255

ATT CGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT  
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser  
1260 1265 1270 1275

GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA  
Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys  
1280 1285 1290

CCA ACG GAA TGG CTT GAT CTT TCT TAT CCG CTT TCT ACT GGA TTT AGA  
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg  
1295 1300 1305

AAT CCT AGT TTT TCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAG AAT  
Asn Pro Ser Phe Ser Glu Met Tyr Gly Trp Arg Tyr Gly Gly Lys Asn  
1310 1315 1320

# FIG.50.

GAC GAG GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA  
Asp Glu Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln  
1325 1330 1335

GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT  
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser  
1340 1345 1350 1355

CAT TTT AGT AAT GCT TAT CGA AAT CTT ATC GGC TTT GCT GAA GAA CTT  
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu  
1360 1365 1370

AGT AAA AAT GGA ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA CAA  
Ser Lys Asn Gly Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala Gln  
1375 1380 1385

AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCA CAA TTA GAT TTT AAT  
Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn  
1390 1395 1400

GGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT  
Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr  
1405 1410 1415

FIG.5P.

AAC CAA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTA GCC TCC  
Asn Gln Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser  
1420 1425 1430 1435  
  
GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC GGT TAT ATC ATT  
Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile  
1440 1445 1450  
  
GGT TTA GCC TAT GAT CAT CCA AGT AAT ACT TCG GGA ATT AAT ACA ATG  
Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met  
1455 1460 1465  
  
TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA AAA CGT  
Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg  
1470 1475 1480  
  
CCA TTA GGT AAC AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT  
Ala Leu Gly Asn Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr  
1485 1490 1495  
  
CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA  
Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys  
1500 1505 1510 1515

**FIG.5Q.**

AAT ATT ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC TAT  
 Asn Ile Met Leu Arg Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr  
 1520 1525 1530  
  
 GTT ACT TGG GAA GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA  
 Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln  
 1535 1540 1545  
  
 CAT CAA AAT GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA AAC  
 His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn  
 1550 1555 1560  
  
 TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAAA TGGGCCAGAT  
 Tyr Thr Leu Thr Leu Glu Met Lys Phe  
 1565 1570  
  
 GGACTAGATA TGCTATATCT ATACCTTACT GGGCATCCT TTTCGTGTTCT ATAATCTGCT  
  
 TAAAGTGAAAA ACCAAACTTG GATTTTITAC AAGATCTTTT CACACATTTA TTGTAAATC  
  
 TCCGACAATT TTGACCG

FIG. 6 A.

AAAAATTCGGT AATGATAACC CTATAAATGA TAAGAGAGAA AGTIGITTTTA CGCCATTTTT  
 CATATTTTAT CCATGAACIT <sup>-35</sup>AAAAAATCT <sup>-10</sup>AAGTTGACAT TATTACAAAA AAAGAACAAT  
 AATGCCGAAT ATTATCAATT TGTATAAGT ATTAAITCT ATG AAA TCT GTA CCT  
 Met Lys Ser Val Pro  
 1 5  
 CTT ATC ACT GGT GGA CTT TCC TTT TTA CTA AGC GCT TGT AGC GGG GGA  
 Leu Ile Thr Gly Gly Leu Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly  
 10 15 20  
 GGT GGT TCT TTT GAT GTA GAT GAC GIC TCT AAT CCC TCC TCT TCT AAA  
 Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn Pro Ser Ser Ser Lys  
 25 30 35  
 CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA AAA TCT GAT TTG  
 Pro Arg Tyr Gln Asp Thr Ser Asn Gln Arg Thr Lys Ser Asp Leu  
 40 45 50  
 GAA AAG TIG TTC ATT OCT TCT TTA GGG GGA GGG ATG AAG TTA GIG GCT  
 Glu Lys Leu Phe Ile Pro Ser Leu Gly Gly Gly Met Lys Leu Val Ala  
 55 60 65

**FIG.6B.**

CAA AAT TTT ATT GGT GCT AGA GAA CCT AGT TTC TTA AAT GAA GAT GGC	
Gln Asn Phe Ile Gly Ala Arg Glu Pro Ser Phe Leu Asn Glu Asp Gly	85
	70
	75
	80
TAT ATG ATA TTT TCC TCA CTT TCT ACG ATT GAA GAG GAT GTT GAA AAA	
Tyr Met Ile Phe Ser Ser Leu Ser Thr Ile Glu Glu Asp Val Glu Lys	100
	90
	95
GTT AAA AAT AAC AAT AAA AAC GGG GGG AGG CTT ATT GGC TCA ATT GAG	
Val Lys Asn Asn Lys Lys Asn Gly Gly Arg Leu Ile Gly Ser Ile Glu	115
	105
	110
GAA CCT AAT GGA ACA TCA CAA AAT TCT AAT TCA CAA GAA TAC GTT TAT	
Glu Pro Asn Gly Thr Ser Gln Asn Ser Asn Ser Gln Glu Tyr Val Tyr	130
	120
	125
TCT GGT TTG TAT TAT ATC GAT AGT TGG CGT GAT TAT AAG AAG GAA GAG	
Ser Gly Leu Tyr Tyr Ile Asp Ser Trp Arg Asp Tyr Lys Lys Glu Glu	145
	135
	140
CAA AAA GCT TAT ACT GGC TAT TAT GGT TAT GCA TTT TAT TAT GGT AAT	
Gln Lys Ala Tyr Thr Gly Tyr Tyr Gly Tyr Ala Phe Tyr Tyr Gly Asn	165
	150
	155
	160

# FIG. 6C.

GAA ACT GCA AAA AAC TTG CCA GTA AAA GGT GTA GCT AAA TAC AAA GGA  
 Glu Thr Ala Lys Asn Leu Pro Val Lys Gly Val Ala Lys Tyr Lys Gly  
 170 175 180

ACG TGG AAC TTC ATC ACT GCA ACT GAA AAT GCC AAA CGT TAT TCT TTG  
 Thr Trp Asn Phe Ile Thr Ala Thr Glu Asn Gly Lys Arg Tyr Ser Leu  
 185 190 195

TTC AGT AAT TCT ATC GGT CAA GCT TAT TCC AGA CGC AGC GCT ATT TCA  
 Phe Ser Asn Ser Ile Gly Gln Ala Tyr Ser Arg Arg Ser Ala Ile Ser  
 200 205 210

GAA GAT ATC TAT AAT TTA GAA AAC GGT GAC GCG GGC TTA ATA AGT GAA  
 Glu Asp Ile Tyr Asn Leu Glu Asn Gly Asp Ala Gly Leu Ile Ser Glu  
 215 220 225

TTT AGT GTA GAT TTT GGT AAG AAA GAG CTC ACT GGA GAA CTT TAT TAT  
 Phe Ser Val Asp Phe Gly Lys Lys Glu Leu Thr Gly Glu Leu Tyr Tyr  
 230 235 240 245

AAT GAA AGG AAA ACA AGT GTT AAT GAA TCA CAA AAT ACA ACA CAT AAA  
 Asn Glu Arg Lys Thr Ser Val Asn Glu Ser Gln Asn Thr Thr His Lys  
 250 255 260



**FIG.6D.**

CTC TAC ACT CTA GAA GCT AAA GTG TAT AGC AAC CGA TTC ACA GGT AAA  
 Leu Tyr Thr Leu Glu Ala Lys Val Tyr Ser Asn Arg Phe Arg Gly Lys  
 265 270 275

GTA AAG CCA ACC AAA ACA AAG TCT GAA GAT CAT CCC TTT ACC AGC GAG  
 Val Lys Pro Thr Lys Thr Lys Ser Glu Asp His Pro Phe Thr Ser Glu  
 280 285 290

CGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT GCT GAA GAA CTA GGG  
 Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn Ala Glu Glu Leu Gly  
 295 300 305

CGA AAG TTT TTA GCT AAC GAC GAA AAA GTT TTT GGG GTA TTT AGT GCC  
 Gly Lys Phe Leu Ala Asn Asp Glu Lys Val Phe Gly Val Phe Ser Ala  
 310 315 320 325

AAA GAA GAC CCA CAA AAC CCA GAA AAC CAA AAA TTA TCC ACA GAA ACC  
 Lys Glu Asp Pro Gln Asn Pro Glu Asn Gln Lys Leu Ser Thr Glu Thr  
 330 335 340

TTA ATT GAT GGC AAG CTA ATT ACT TTT AAA AGA ACT GAT GCA ACA ACC  
 Leu Ile Asp Gly Lys Leu Ile Thr Phe Lys Arg Thr Asp Ala Thr Thr  
 345 350 355

## FIG.6E.

AAT GCA ACA ACC GAT GCA AAA ACC AGT GCA ACA ACC GAT GCA ACC AGT  
 Asn Ala Thr Thr Asp Ala Lys Thr Ser Ala Thr Thr Asp Ala Thr Ser  
 360 365 370

ACA ACA GCC AAT AAA ACC GAT GCA GAA AAC TTT AAG ACG GAA GAT  
 Thr Thr Ala Asn Lys Lys Thr Asp Ala Glu Asn Phe Lys Thr Glu Asp  
 375 380 385

ATA CCA AGT TTT GGT GAA GCT GAT TAC CTT TTA ATT GGC AAT CAG CCT  
 Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Ile Gly Asn Gln Pro  
 390 395 400 405

ATT CCT CTT TTA CCT GAA AAA AAT ACT GAT GAT TTC ATA AGT AGT AAG  
 Ile Pro Leu Leu Pro Glu Lys Asn Thr Asp Asp Phe Ile Ser Ser Lys  
 410 415 420

CAC CAT ACG GTA GGA GGT AAA ACC TAT AAA GTA GAA GCA TGT TGC AAG  
 His His Thr Val Gly Gly Lys Thr Tyr Lys Val Glu Ala Cys Cys Lys  
 425 430 435

AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT GAG GAT AAA GAT AAG  
 Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys Asp Lys  
 440 445 450

**FIG.6F.**

GAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GGC AAA GAA AAA CCA ACG  
 Asp Asn Lys Asn Glu Thr 460  
 455  
 ACG ACA ACA TCT ATC AAC ACT TAT TAT CAA TTC TTA TTA GGT CTC CGT  
 Thr Thr Thr Ser Ile Asn Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg  
 470  
 475  
 480  
 485  
 ACT CCC AAG GAC GAA ATA CCT AAA GAA GGA AGT GCA AAA TAT CAT GGT  
 Thr Pro Lys Asp Glu Ile Pro Lys Glu Gly Ser Ala Lys Tyr His Gly  
 490  
 495  
 500  
 AAT TGG TTT GGT TAT ATT AGT GAT GGC GAG ACA TCT TAC TCC GCC AGT  
 Asn Trp Phe Gly Tyr Ile Ser Asp Gly Glu Thr Ser Tyr Ser Ala Ser  
 505  
 510  
 515  
 GGT GAT AAG GAA CGC AGT AAA AAT GCT GTC GCC GAG TTT GAT GTA AGT  
 Gly Asp Lys Glu Arg Ser Lys Asn Ala Val Ala Glu Phe Asp Val Ser  
 520  
 525  
 530  
 TTT GCC AAT AAA ACA TTA ACA GGC GAA TTA AAA CGA CAC GAT AAT GGA  
 Phe Ala Asn Lys Thr Leu Thr Gly Glu Leu Lys Arg His Asp Asn Gly  
 535  
 540  
 545

# FIG. 6G.

AAT ACC GTA TTT AAA ATT AAT GCA GAA TTA AAT GGT AGT AAT GAC TTC  
 Asn Thr Val Phe Lys Ile Asn Ala Glu Leu Asn Gly Ser Asn Asp Phe  
 550 555 560

ACT GGT ACA GCA ACC GCA ACA AAT TTT GTA ATA GAT GGT AAC AAT AGT  
 Thr Gly Thr Ala Thr Ala Thr Asn Phe Val Ile Asp Gly Asn Asn Ser  
 570 575 580

CAA ACT TCA AAT GCC AAA ATT AAT ATT ACA ACT AAA GTA AAT GGG GCA  
 Gln Thr Ser Asn Ala Lys Ile Asn Ile Thr Thr Lys Val Asn Gly Ala  
 585 590 595

TTT TAT GGA CCT AAG GCT TCT GAA TTA GGA GGG TAT TTC ACC TAT AAC  
 Phe Tyr Gly Pro Lys Ala Ser Glu Leu Gly Gly Tyr Phe Thr Tyr Asn  
 600 605 610

GGA AAA AAT CCT ACA GCT ACA AAT TCT GAA AGT TCC TCA ACC GTA CCT  
 Gly Lys Asn Pro Thr Ala Thr Asn Ser Glu Ser Ser Ser Thr Val Pro  
 615 620 625

TCA CCA CCC AAT TCA CCA AAT GCA AGC GCT GCA GTT GTC TTT GGT GCT  
 Ser Pro Pro Asn Ser Pro Asn Ala Ser Ala Ala Val Val Phe Gly Ala  
 630 635 640 645

# FIG.6H.

AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAAACAAC CAAGTAATGG  
Lys Lys Gln Val Glu Thr Thr Asn Lys  
650

AATACTAAAA ATG ACT AAA AAA CCC TAT TTT CGC CTA AGT ATT ATT TCT  
Met Thr Lys Lys Pro Tyr Phe Arg Leu Ser Ile Ile Ser  
655 660 665

TGT CTT TTA ATT TCA TGC TAT GTA AAA GCA GAA ACT CAA AGT ATA AAA  
Cys Leu Leu Ile Ser Cys Tyr Val Lys Ala Glu Thr Gln Ser Ile Lys  
670 675 680

GAT ACA AAA GAA GCT ATA TCA TCT GAA GTG GAC ACT CAA AGT ACA GAA  
Asp Thr Lys Glu Ala Ile Ser Ser Glu Val Asp Thr Gln Ser Thr Glu  
685 690 695

GAT TCA GAA TTA GAA ACT ATC TCA GTC ACT GCA GAA AAA ATA AGA GAT  
Asp Ser Glu Leu Glu Thr Ile Ser Val Thr Ala Glu Lys Ile Arg Asp  
700 705 710 715

CGT AAA GAT AAT GAA GTA ACT GCA CTT GGC AAA ATT ATC AAA ACT AGT  
Arg Lys Asp Asn Glu Val Thr Gly Leu Gly Lys Ile Ile Lys Thr Ser  
720 725 730

FIG. 61.

GAA AGT ATC AGC CGA GAA CAA GTA TTA AAT ATT CGT GAT CTA ACA CGC  
 Glu Ser Ile Ser Arg Glu Gln Val Leu Asn Ile Arg Asp Leu Thr Arg  
 735 740 745

TAT GAT CCA GGC ATT TCA GTT GTA GAA CAA GGC CGT GGT GCA AGT TCT  
 Tyr Asp Pro Gly Ile Ser Val Val Glu Gln Gly Arg Gly Ala Ser Ser  
 750 755 760

CGA TAT TCT ATT CGT GGT ATG GAC AGA AAT AGA GTT GCT TTA TTA GTA  
 Gly Tyr Ser Ile Arg Gly Met Asp Arg Asn Arg Val Ala Leu Leu Val  
 765 770 775

GAT GGT TTA CCT CAA ACG CAA TCT TAT GTA GTG CAA AGC CCT TTA GTT  
 Asp Gly Leu Pro Gln Thr Gln Ser Tyr Val Val Gln Ser Pro Leu Val  
 780 785 790 795

GCT CGT TCA GGA TAT TCT GGC ACT GGT GCA ATT AAT GAA ATT GAA TAT  
 Ala Arg Ser Gly Tyr Ser Ser Gly Thr Gly Ala Ile Asn Glu Ile Glu Tyr  
 800 805 810

GAA AAT GTA AAG GCC GTC GAA ATA AGC AAG GGG AGT TCT TCT GAG  
 Glu Asn Val Lys Ala Val Glu Ile Ser Lys Gly Gly Ser Ser Ser Glu  
 815 820 825

## FIG.6J.

TAT GGT AAT GGA GCA CTA GCT GGT TCT GTA ACA TTT CAA AGC AAA TCA  
 Tyr Gly Asn Gly Ala Leu Ala Gly Ser Val Thr Phe Gln Ser Lys Ser  
 830 840  
  
 GCA GCC GAT ATC TTA GAA GGA GAC AAA TCA TGG GGA ATT CAA ACT AAA  
 Ala Ala Asp Ile Leu Glu Gly Asp Lys Ser Trp Gly Ile Gln Thr Lys  
 845 855  
  
 AAT GCT TAT TCA AGC AAA AAT AAA GGC TTT ACC CAT TCT TTA GCT GTA  
 Asn Ala Tyr Ser Ser Lys Asn Lys Gly Phe Thr His Ser Leu Ala Val  
 860 865 870 875  
  
 GCT GGA AAA CAA GGG GGA TTT GAC GGG GTC GCC ATT TAT ACT CAA CGA  
 Ala Gly Lys Gln Gly Gly Phe Asp Gly Val Ala Ile Tyr Thr Gln Arg  
 880 885 890  
  
 AAT TCA ATT GAA ACC CAA GTC CAT AAA GAT GCA TTA AAA GGC GTA CAA  
 Asn Ser Ile Glu Thr Gln Val His Lys Asp Ala Leu Lys Gly Val Gln  
 895 900 905  
  
 AGT TAT CAT CGA TTA ATC GCC AAA CCA GAG GAT CAA TCT GCA TAC TTT  
 Ser Tyr His Arg Leu Ile Ala Lys Pro Glu Asp Gln Ser Ala Tyr Phe  
 910 915 920

# FIG. 6K.

GTG ATG CAA GAT GAG TGT CCA AAG CCA GAT GAT TAT AAC AGT TGT TTA  
Val Met Gln Asp Glu Cys Pro Lys Pro Asp Asp Tyr Asn Ser Cys Leu  
925 930

CCT TTC GCC AAA CGA CCT GCG ATT TTA TCC CAA AGA GAA ACC GTA  
Pro Phe Ala Lys Arg Pro Ala Ile Leu Ser Ser Gln Arg Glu Thr Val  
940 945 950 955

AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA CCT AAT CCA ATG  
Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys Pro Asn Pro Met  
960 965 970

AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG TAT CAT TTT TCT  
Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Tyr His Phe Ser  
975 980 985

GAA CAA CAT TAT ATT GGT GGT ATT TTT GAA TTC ACA CAA AAA TTT  
Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr Gln Gln Lys Phe  
990 995 1000

GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA TCA ACA GAA AAA  
Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg Ser Thr Glu Lys  
1005 1010 1015



## FIG.6L.

CCG GAT GAT AGC AGT GGC TCT TTT TAT CCA AAG CAA GAT TAT GGT GCA  
 Arg Asp Asp Ser Ser Gly Ser Phe Tyr Pro Lys Gln Asp Tyr Gly Ala  
 1020 1025 1030 1035  
  
 TAT CAA CGT ATT GAG GAT GGC CGA GGC GTT AAC TAT GCA AGT GGG CTT  
 Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr Ala Ser Gly Leu  
 1040 1045 1050  
  
 TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA CGT ATT GAA TAT ATT  
 Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly Ile Glu Tyr Ile  
 1055 1060 1065  
  
 TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA GCA GIG TTA AGT  
 Tyr Glu Asn Lys Lys Asn Lys Ala Gly Ile Ile Asp Lys Ala Val Leu Ser  
 1070 1075 1080  
  
 GCT AAT CAA CAA AAC ATC ATA CTT GAC AGT TAT ATG CAA CAT ACG CAT  
 Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met Gln His Thr His  
 1085 1090 1095  
  
 TGC AGT CTT TAT CCT AAT CCA AGT AAG AAT TGC CGC CCA ACA CGT GAT  
 Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg Pro Thr Arg Asp  
 1100 1105 1110 1115

## FIG. 6M.

AAA CCT TAT TCA TAC TAT CAT TCT GAT AGA AAT GTT TAT AAA GAA AAA  
Lys Pro Tyr Ser Tyr Tyr His Ser Asp Arg Asn Val Tyr Lys Glu Lys  
1120 1125 1130

CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT CAA CAA AAT TGG  
His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile Gln Gln Asn Trp  
1135 1140 1145

CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT GAC TTT ACT TCA  
Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp Asp Phe Thr Ser  
1150 1155 1160

GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT ACC GCT ACG GCA  
Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val Thr Ala Thr Ala  
1165 1170 1175

AAG AGT ATT TCA GAG AAA GCT AAT GAA ACA AGA AAT GGT TAC AAA  
Lys Ser Ile Ser Glu Lys Ala Asn Glu Thr Arg Arg Asn Gly Tyr Lys  
1180 1185 1190 1195

AAA CAA CCT TAC TTA TAC CCA AAA CCA ACA GTA GGT TTT GTA GTA CAA  
Lys Gln Pro Tyr Leu Tyr Pro Lys Pro Thr Val Gly Phe Val Val Gln  
1200 1205 1210

# FIG.6N.

GAT CAT TGT GAT TAT AAA GGT AAC TCC TCT AAT TAC AGA GAC TGT AAA  
Asp His Cys Asp Tyr Lys Gly Asn Ser Ser Asn Tyr Arg Asp Cys Lys  
1215 1220 1225

GTG CCG TTA ATT AAA GGG AAA AAT TAT TTC GCA GCA CGC AAT AAT  
Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala Ala Arg Asn Asn  
1230 1235 1240

ATG GCA TTA GGG AAA TAC GTT GAT TTA GGT TTA GGT ATT CGG TAT GAC  
Met Ala Leu Gly Lys Tyr Val Asp Leu Gly Leu Gly Ile Arg Tyr Asp  
1245 1250 1255

GTA TCT CGC ACA AAA GCT AAT GAA TCA ACT ATT AGT GTT GGT AAA TTT  
Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser Val Gly Lys Phe  
1260 1265 1270 1275

AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA CCA ACG GAA TGG  
Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys Pro Thr Glu Trp  
1280 1285 1290

CIT GAT CTT TCT TAT CGC CTT TCT ACT CGA TTT AGA AAT CCT AGT TTT  
Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg Asn Pro Ser Phe  
1295 1300 1305

## FIG.60.

GCT GAA ATG TAT GGT TGG CGG TAT GGT GGC AAT AAT AGC GAG GTT TAT  
 Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Ser Glu Val Tyr  
 1310 1315 1320  
  
 GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA GAG TTT GGT CTC  
 Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln Glu Phe Gly Leu  
 1325 1330 1335  
  
 GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT CAT TTT AGT AAT  
 Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser His Phe Ser Asn  
 1340 1345 1350 1355  
  
 GCT TAT CGA AAT CTT ATC GCC TTT GCT GAA GAA CTT AAT AAA AAT GGA  
 Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu Asn Lys Asn Gly  
 1360 1365 1370  
  
 ACT GGA AAG GCC AAT TAT GGA TAT CAT AAT GCA CAA AAT GCA AAA TTA  
 Thr Gly Lys Ala Asn Tyr Gly Tyr His Asn Ala Gln Asn Ala Lys Leu  
 1375 1380 1385  
  
 GTT GGC GTA AAT ATA ACT CGG CAA TTA GAT TTT AAT GGT TTA TGG AAA  
 Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe Asn Gly Leu Trp Lys  
 1390 1395 1400

## FIG.6P.

CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT TAT AAC CGA GTA AAA  
 Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala Tyr Asn Arg Val Lys  
 1405 1410 1415

GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC TCC GTA AGC AGT TAT  
 Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala Ser Val Ser Ser Tyr  
 1420 1425 1430 1435

TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC ATT GGT TTA GCC TAT  
 Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile Ile Gly Leu Gly Tyr  
 1440 1445 1450

GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA ATG TTT ACT CAA TCA  
 Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr Met Phe Thr Gln Ser  
 1455 1460 1465

AAA GCA AAA TCT CAA AAT GAA TTG CTA GCA AAA CGT GCA TTG GGT AAC  
 Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Lys Arg Ala Leu Gly Asn  
 1470 1475 1480

AAT TCA AGG GAT GTA AAA TCA ACA AGA AAA CTT ACT CGG GCA TGG CAT  
 Asn Ser Arg Asp Val Lys Ser Thr Arg Lys Leu Thr Arg Ala Trp His  
 1485 1490 1495

# FIG.6Q.

ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT AAA AAT ATT ATG CTT  
 Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn Lys Asn Ile Met Leu  
 1500 1505 1510 1515

CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT GCG TAT GTT ACT TGG GAA  
 Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg Tyr Val Thr Trp Glu  
 1520 1525 1530

GCG GTG CGT CAA ACA GCA CAA GGT GCG GTC AAT CAA CAT CAA AAT GTT  
 Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn Gln His Gln Asn Val  
 1535 1540 1545

GGT AGC TAT ACT CGC TAC GCA GCA TCA GCA AAC TAT ACC TTA ACA  
 Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg Asn Tyr Thr Leu Thr  
 1550 1555 1560

TTA GAA ATG AAA TTCTAAATTA AAATGGGCCA GATGGACTAG ACATGCTATA  
 Leu Glu Met Lys  
 1565

TCTATACCTT ACIGGGGCAT CTTTTCIGT TCTATAATCT GGTTAAGTGA AAAACCAAC

TTGGATTTTT TAGAAGATCT TTCCACGCAT TTATTGTAAA ATCTCCGACA ATTTTACCG

CACTTTCTC TATTACAAA ACAATAAGGA TCCTTTTIGT AATCTCTCA

FIG. 7 A.

```

CAACATCTGC CCAAGCTATA TTGTTTAATG ATAAGCCTAT TAATGATAAG CCTATTAAATG
ATAAGAAAAGA AATTGTGTTT ACGCCATTTT TCATATTTTA TCCATGAACT TAAAAAATTC
TAAGTIGACA TTATTACAAA AAAAGAACAA TAATCGCAAT TATTATCAAT TTGTGATAAG
AATATAATTC T ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe
1      5      10
TTA TTA AGT GCT TCT AGC GGA GGA GGT TCT TTT GAT GTA GAT AAC GTC
Leu Leu Ser Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val
15      20      25
TCT AAT CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT
Ser Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn
30      35      40      45
CAA AGA ACA AAA TCT GAT TTG CAA AAG TTG TCC ATT CCT TCT TTA GGG
Gln Arg Thr Lys Ser Asp Leu Gln Lys Leu Ser Ile Pro Ser Leu Gly
50      55      60

```

## FIG.7B.

GGA GGG ATG AAG TTA GTG GCT CAG AAT CTT CTT GGT AAG AAA GAA CCT  
 Gly Gly Met Lys Leu Val Ala Gln Asn Leu Leu Gly Lys Lys Glu Pro  
 65 70 75  
 AGT CTC TTA AAT AAT GAA GAT GGC TAT ATG ATA TTT TCC TCA CTT TCT  
 Ser Leu Leu Asn Asn Glu Asp Gly Tyr Met Ile Phe Ser Ser Leu Ser  
 80 85 90  
 ACG ATT GAA GAG GAT GTT ACA AAA GAA AAT AAA TCT CAG GAA CCC ACT  
 Thr Ile Glu Glu Asp Val Thr Lys Glu Asn Lys Ser Gln Glu Pro Thr  
 95 100 105  
 ATT GGC TCA ATA GAC GAG CCT AGC AAA ACA AAT TCA CCC CAA AAT CAT  
 Ile Gly Ser Ile Asp Glu Pro Ser Lys Thr Asn Ser Pro Gln Asn His  
 110 115 120 125  
 CAT GGC AAT ATG TAT ATT CCG GTC TTT ATT ATA TTC AAT CGT GGC GTA  
 His Gly Asn Met Tyr Ile Arg Val Phe Ile Ile Phe Asn Arg Gly Val  
 130 135 140  
 ATT CCT CAA ATG GCA AGT TTT ATT CAG GTT ACT ATG GAT ATG CGT ATT  
 Ile Pro Gln Met Ala Ser Phe Ile Gln Val Thr Met Asp Met Arg Ile  
 145 150 155



## FIG. 7 C.

ACT TTG GCA AGC AAA CAG CCA CTA CAT TAC CTG TAGATGGCGA AGCAACGTAT  
 Thr Leu Ala Ser Lys Gln Pro Leu His Tyr Leu  
 160 165

AAAGGAACIT GGCACITCAT CACCGCAACT GAAAATGGCA AAAAGTATTC TTGTTCACGT  
 AATGATAGCG GTCAAGCTTA TCGCAGACGT AGTCCAATTC CAGAAGATAT TGATTTAGAA  
 AAAAAATGATT CAACTAATGG TGACAAGGGC TTAATAAGTG AATTIAGIGT CAATTTTGGT  
 ACAAAAAGC TCACTGGAAA ACTTTATTAT AATGAAAAGAG AAACAGAACT TAATAAATCA  
 AAAGATAGAA AACATACACT CTACAACTTA GAAGCTGAAG TGTATAGTAA CCGATTICAGG  
 CGTACAGTAA AGCCAACCGA AAAAGATICT ACAGATCATC CCTTTACCAG CGAGGGAACA  
 TTAGAAGGIG GTTTTATATG GCCTAAAGGT GAAGAAGTAG GAGGAAAGTT TTTAGCTGGC  
 GATAAAAAAG TTTTITGGGT ATTTIAGIGCC AAAGAAAACGG AAGAAAACAAA AAAGAAAACGG  
 TTATCCAAGG AAACCTTAAT TGATGGCAAG CTAACTACTT TTAATAACAAC CAATGCCACA  
 ACCAATGCAA CAGCCAATGC AACCAACAGT ACAACAGCCA GTACAACAAC CGATGCAGAA

**FIG. 7D.**

AACTTTACGA CGAAAGATAT ACCAAGTTTT GGTAAGCIG ATTACCTTTT AATTCATAAT  
TACCCTGTTC CTCCTTTACC TCAGAGTGGT GATTTCATAA GTAGTAAGCA CCATACIGTA  
CGAAAGAAA CCTATCAAGT AGAAGCATGT TCCAGTAATC TAAGCTATGT GAAATTTGGT  
ATGTTTTATG AAGACCCACT TAAAGAAGAA AAAGACAAG AAAAAGAAGA AGACAAAGAA  
AAACAAACGG CCGCAACGAC CAACACTTAT TATCAATTCT TATTAGGICT CCGTACIGCC  
AGTTCIGAAA TTCTTAAAT GGGAAACGIG GAATATCGCG GTAATTGGIT TGGTTATATT  
AGTCATGGCA CGACATCTTA CTCCTCCAGT GGTGATAAG AACGCAATAA AAATGCTCCC  
GCCGATTTTA ATGTTCATTT TGTCAATAAA AAGCTAACAG GCACATTAAA ACGACACGAT  
AATGGAAATA CCGTATTTAG TATTGAGGCA AACTTTAACA GTGGGAATGA CTTCACITGGT  
AAAGCAACCG CAAAAGATTT AGTAATAGAT GGTAAAAGTA CACAAGCCAC ATCTAAAGTC  
AATTTACGG CAACAGTAAA AGGGCATTTT TATGGACCIG ATGCTTCIGA ATTAGGCGGT  
TATTTACCT ATAACGGAAA AAATCCTACA GCTACAAATT CCCCACCCGT ATCTTCACCA

FIG.7E.

TCCAATTACAG CAAATGCTCG TGCTGCCGTT GTCGTTGGAG CTAAAAACA AGTAGACACA

ACCAACAAGT AGAAAAAACC AAATAATCGA ATACTAAAA ATG ACT AAA AAA CCC  
Met Thr Lys Lys Pro  
170

TAT TTT CGC CTA AGT ATT ATT TCT TGT CTT TTA ATT TCA TGC TAT GTA  
Tyr Phe Arg Leu Ser Ile Ile Ser Cys Leu Leu Ile Ser Cys Tyr Val  
175 180 185

AAA GCA GAA ACT CAA AGT ATA AAA GAT ACA AAA GAA GCT ATA TCA TCT  
Lys Ala Glu Thr Gln Ser Ile Lys Asp Thr Lys Glu Ala Ile Ser Ser  
190 195 200 205

GAA GTG GAC ACT CAA AGT ACA GAA GAT TCA GAA TTA GAA ACT ATC TCA  
Glu Val Asp Thr Gln Ser Thr Glu Asp Ser Glu Leu Glu Thr Ile Ser  
210 215 220

GTC ACT GCA GAA AAA ATA AGA GAT CGT AAA GAT AAT GAA GTA ACT GGA  
Val Thr Ala Glu Lys Ile Arg Asp Arg Lys Asp Asn Glu Val Thr Gly  
225 230 235

CTT GGC AAA ATT ATA AAA ACG AGT GAA AGT ATC AGC CGA GAA CAA GTA  
Leu Gly Lys Ile Ile Lys Thr Ser Glu Ser Ile Ser Arg Glu Gln Val  
240 245 250

FIG.7F.

TTA AAT ATT CGT GAT CTA ACA CGC TAT GAT CCA GGC ATT TCA GTT GTA  
 Leu Asn Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val  
 255 260 265

GAA CAA GGT CGC GGT GCA AGT TCT GGA TAT TCT ATT CGT GGT ATG GAC  
 Glu Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ser Ile Arg Gly Met Asp  
 270 275 280 285

AGA AAT AGA GTT GCT TTA TTA GTA GAT GGT TTA CCT CAA ACG CAA TCT  
 Arg Asn Arg Val Ala Leu Leu Val Asp Gly Leu Pro Gln Thr Gln Ser  
 290 295 300

TAT GTA GTG CAA AGC CCT TTA GTT GCT CGT TCA GGA TAT TCT GGC ACT  
 Tyr Val Val Gln Ser Pro Leu Val Ala Arg Ser Gly Tyr Ser Gly Thr  
 305 310 315

GGT GCA ATT AAT GAA ATT GAA TAT GAA AAT GTA AAG GCC GTC GAA ATA  
 Gly Ala Ile Asn Glu Ile Glu Tyr Glu Asn Val Lys Ala Val Glu Ile  
 320 325 330

AGC AAG GGG GGG AGT TCT TCT GAG TAT GGT AAT GGA GCA CTA GCT GGT  
 Ser Lys Gly Gly Ser Ser Ser Glu Tyr Gly Asn Gly Ala Leu Ala Gly  
 335 340 345

FIG. 76.

TCT GTA ACA TTT CAA AGC AAA TCC GCA GCC GAT ATC TTA GAA GGA GAC	
Ser Val Thr Phe Gln Ser Lys Ser Ala Ala Asp Ile Leu Glu Gly Asp	365
350	360
AAA TCA TGG GGA ATT CAA ACT AAA AAT GCT TAT TCA AGC AAA AAT AAA	
Lys Ser Trp Gly Ile Gln Thr Lys Asn Ala Tyr Ser Ser Lys Asn Lys	380
370	375
GGC TTT ACC CAT TCT TTA GCT GTA GCA GGA AAA CAA GGT GGA TTT GAA	
Gly Phe Thr His Ser Leu Ala Val Ala Gly Lys Gln Gly Gly Phe Glu	395
385	390
GGG GTC GCC ATT TAC ACT CAA CGA AAT TCG GAG GAA ACC CAA GTC CAT	
Gly Val Ala Ile Tyr Thr Gln Arg Asn Ser Glu Glu Thr Gln Val His	410
400	405
AAA GAT GCA TTA AAA GGC GTA CAA AGT TAT GAG CGA TTC ATC GCC ACA	
Lys Asp Ala Leu Lys Gly Val Gln Ser Tyr Glu Arg Phe Ile Ala Thr	425
415	420
ACA GAT AAA TCT TCA GGA TAC TTT GTG ATA CAA GGT GAG TGT CCA AAT	
Thr Asp Lys Ser Ser Gly Tyr Phe Val Ile Gln Gly Glu Cys Pro Asn	445
430	435

## FIG.7H.

GGT GAT GAC AAG TGT GCA GCC AAA CCA CCT GCA AAG TTA TCC CCC CAA  
 Gly Asp Asp Lys Cys Ala Ala Lys Pro Pro Ala Lys Leu Ser Pro Gln  
 450 455 460

AGC GAA ACC GTA AGC GTT TCA GAT TAT ACG GCG GCT AAC CGT ATC AAA  
 Ser Glu Thr Val Ser Val Ser Asp Tyr Thr Gly Ala Asn Arg Ile Lys  
 465 470 475

CCT AAT CCA ATG AAA TAT GAA AGC CAG TCT TGG TTT TTA AGA GGA GGG  
 Pro Asn Pro Met Lys Tyr Glu Ser Gln Ser Trp Phe Leu Arg Gly Gly  
 480 485 490

TAT CAT TTT TCT GAA CAA CAC TAT ATT GGT GGT ATT TTT GAA TTC ACA  
 Tyr His Phe Ser Glu Gln His Tyr Ile Gly Gly Ile Phe Glu Phe Thr  
 495 500 505

CAA CAA AAA TTT GAT ATC CGT GAT ATG ACA TTT CCC GCT TAT TTA AGA  
 Gln Gln Lys Phe Asp Ile Arg Asp Met Thr Phe Pro Ala Tyr Leu Arg  
 510 515 520 525

TCA ACA GAA AAA CCG GAT GAT AGA ACT GCG CCT TTT TAT CCA AAG CAA  
 Ser Thr Glu Lys Arg Asp Arg Thr Gly Pro Phe Tyr Pro Lys Gln  
 530 535 540

FIG. 71.

GAT TAT GGT GCA TAT CAA CGT ATT GAG GAT GGC CGA GGC GTT AAC TAT	
Asp Tyr Gly Ala Tyr Gln Arg Ile Glu Asp Gly Arg Gly Val Asn Tyr	545 550 555
GCA AGT GGG CTT TAT TTC GAT GAA CAC CAT AGA AAA CAG CGT GTA GGT	
Ala Ser Gly Leu Tyr Phe Asp Glu His His Arg Lys Gln Arg Val Gly	560 565 570
ATT GAA TAT ATT TAC GAA AAT AAG AAC AAA GCG GGC ATC ATT GAC AAA	
Ile Glu Tyr Ile Tyr Glu Asn Lys Asn Lys Ala Gly Ile Ile Asp Lys	575 580 585
GCA GTG TTA AGT GCT AAT CAA CAA AAC AAC ATC ATA CTT GAC AGT TAT ATG	
Ala Val Leu Ser Ala Asn Gln Gln Asn Ile Ile Leu Asp Ser Tyr Met	590 595 600 605
CGA CAT ACG CAT TGC AGT CTT TAT OCT AAT CCA AGT AAG AAT TGC CGC	
Arg His Thr His Cys Ser Leu Tyr Pro Asn Pro Ser Lys Asn Cys Arg	610 615 620
CCG ACA CTT GAT AAA CCT TAT TCA TAC TAT CGT TCT GAT AGA AAT GTT	
Pro Thr Leu Asp Lys Pro Tyr Ser Tyr Tyr Arg Ser Asp Arg Asn Val	625 630 635

## FIG.7 J.

TAT AAA GAA AAA CAT AAT ATG TTG CAA TTG AAT TTA GAG AAA AAA ATT  
Tyr Lys Glu Lys His Asn Met Leu Gln Leu Asn Leu Glu Lys Lys Ile  
640 645 650

CAA CAA AAT TGG CTT ACT CAT CAA ATT GTC TTC AAT CTT GGT TTT GAT  
Gln Gln Asn Trp Leu Thr His Gln Ile Val Phe Asn Leu Gly Phe Asp  
655 660 665

GAC TTT ACT TCA GCG CTT CAG CAT AAA GAT TAT TTA ACT CGA CGT GTT  
Asp Phe Thr Ser Ala Leu Gln His Lys Asp Tyr Leu Thr Arg Arg Val  
670 675 680 685

ACC GCT ACG GCA AAT ATT ATT TCA GGG ACA GTT GCT GGT AAA CGA AGA  
Thr Ala Thr Ala Asn Ile Ile Ser Gly Thr Val Ala Gly Lys Arg Arg  
690 695 700

AAT GGT TAC GAA AAA CAA CCT TAC TTA TAC TCA AAA CCA AAA GTA GAT  
Asn Gly Tyr Glu Lys Lys Gln Pro Tyr Leu Tyr Ser Lys Pro Lys Val Asp  
705 710 715

TTT GTA GGA CAA GAT CAT TGT AAT TAT AAA GGT AGC TCC TCT AAT TAC  
Phe Val Gly Gln Asp His Cys Asn Tyr Lys Gly Ser Ser Ser Asn Tyr  
720 725 730



FIG.7K.

AGC GAC TGT AAA GIG CCG TTA ATT AAA GGG AAA AAT TAT TAT TTC GCA	
Ser Asp Cys Lys Val Arg Leu Ile Lys Gly Lys Asn Tyr Tyr Phe Ala	
	735 740 745
GCA CGC AAT AAT ATG GCA TTA GGG AAA TAC ATT GAT TTA GGT TTA GGT	
Ala Arg Asn Asn Met Ala Leu Gly Lys Tyr Ile Asp Leu Gly Leu Gly	
	750 755 760 765
ATT CGG TAT GAC GTA TCT CGT ACA AAA GCT AAT GAA TCA ACT ATT AGT	
Ile Arg Tyr Asp Val Ser Arg Thr Lys Ala Asn Glu Ser Thr Ile Ser	
	770 775 780
GTT GGT AAA TTT AAA AAT TTC TCT TGG AAT ACT GGT ATT GTC ATA AAA	
Val Gly Lys Phe Lys Asn Phe Ser Trp Asn Thr Gly Ile Val Ile Lys	
	785 790 795
CCA ACG GAA TGG CTT GAT CTT TCT TAT CCG CTT TCT ACT GGA TTT AGA	
Pro Thr Glu Trp Leu Asp Leu Ser Tyr Arg Leu Ser Thr Gly Phe Arg	
	800 805 810
AAT CCT AGT TTT GCT GAA ATG TAT GGT TGG CCG TAT GGT GGC AAT AAT	
Asn Pro Ser Phe Ala Glu Met Tyr Gly Trp Arg Tyr Gly Gly Asn Asn	
	815 820 825

**FIG. 7L:**

AGC GAT GTT TAT GTA GGT AAA TTT AAG CCT GAA ACA TCT CGT AAC CAA  
Ser Asp Val Tyr Val Gly Lys Phe Lys Pro Glu Thr Ser Arg Asn Gln  
830 835 840 845

GAG TTT GGT CTC GCT CTA AAA GGG GAT TTT GGT AAT ATT GAG ATC AGT  
Glu Phe Gly Leu Ala Leu Lys Gly Asp Phe Gly Asn Ile Glu Ile Ser

CAT TTT AGT AAT GCT TAT TAT CGA AAT CTT ATC GGC TTT GCT GAA GAA CTT  
His Phe Ser Asn Ala Tyr Arg Asn Leu Ile Ala Phe Ala Glu Glu Leu 865 870 875

AGT AAA AAT GGA ACT ACT GGA AAG GGC AAT TAT GGA TAT CAT AAT GCA  
Ser Lys Asn Gly Thr Thr Gly Lys Gly Asn Tyr Gly Tyr His Asn Ala

CAA AAT GCA AAA TTA GTT GGC GTA AAT ATA ACT GCG CAA TTA GAT TTTT  
Gln Asn Ala Lys Leu Val Gly Val Asn Ile Thr Ala Gln Leu Asp Phe 905  
895 900

AAT CGT TTA TGG AAA CGT ATT CCC TAC GGT TGG TAT GCA ACA TTT GCT  
Asn Gly Leu Trp Lys Arg Ile Pro Tyr Gly Trp Tyr Ala Thr Phe Ala  
910 915 920 925

## FIG.7M.

TAT AAC CGA GTA AAA GTT AAA GAT CAA AAA ATC AAT GCT GGT TTG GCC  
 Tyr Asn Arg Val Lys Val Lys Asp Gln Lys Ile Asn Ala Gly Leu Ala  
 930 935 940  
 TCC GTA AGC AGT TAT TTA TTT GAT GCC ATT CAG CCC AGC CGT TAT ATC  
 Ser Val Ser Ser Tyr Leu Phe Asp Ala Ile Gln Pro Ser Arg Tyr Ile  
 945 950 955  
 ATT GGT TTA GGC TAT GAT CAT CCA AGT AAT ACT TGG GGA ATT AAT ACA  
 Ile Gly Leu Gly Tyr Asp His Pro Ser Asn Thr Trp Gly Ile Asn Thr  
 960 965 970  
 ATG TTT ACT CAA TCA AAA GCA AAA TCT CAA AAT GAA TTG CTA GGA CAA  
 Met Phe Thr Gln Ser Lys Ala Lys Ser Gln Asn Glu Leu Leu Gly Gln  
 975 980 985  
 CGT GCA TTG GGT AAC AAT TCA AGG AAT GTA AAA TCA ACA AGA AAA CTT  
 Arg Ala Leu Gly Asn Asn Ser Arg Asn Val Lys Ser Thr Arg Lys Leu  
 990 995 1000 1005  
 ACT CGG GCA TGG CAT ATC TTA GAT GTA TCG GGT TAT TAC ATG GCG AAT  
 Thr Arg Ala Trp His Ile Leu Asp Val Ser Gly Tyr Tyr Met Ala Asn  
 1010 1015 1020

# FIG.7N.

AAA AAT ATT ATG CTT CGA TTA GGG ATA TAT AAT TTA TTC AAC TAT CGC  
Lys Asn Ile Met Leu Arg Leu Gly Ile Tyr Asn Leu Phe Asn Tyr Arg  
1025 1030 1035

TAT GTT ACT TGG GAA GCG GIG CGT CAA ACA GCA CAA GGT GCG GTC AAT  
Tyr Val Thr Trp Glu Ala Val Arg Gln Thr Ala Gln Gly Ala Val Asn  
1040 1045 1050

CAA CAT CAA AAT GTT GGT AGC TAT ACT CGC TAC GCA GCA TCA GGA CGA  
Gln His Gln Asn Val Gly Ser Tyr Thr Arg Tyr Ala Ala Ser Gly Arg  
1055 1060 1065

AAC TAT ACC TTA ACA TTA GAA ATG AAA TTC TAAATTAAAA TCGGCCAGAT  
Asn Tyr Thr Leu Thr Leu Glu Met Lys Phe  
1070 1075

GGACTAGATA TGCTATATCT ATACCTTACT GGGGCATCTT TTCTGTCTCT ATAATCTGCT

TAAAGTCAAAA ACCAAACTTG GATTTTTHAC AAGATCTTTT CACGCATTTA TTGTAAAATC

TCCGACAAAT TTATACCGCAC TTTTCTCTAT TACAAAAACA ATAAGGATCC TTTTGTGACT

CTCTCAATCT TTGGCAAGTT GCTGTTHACAA CTTCAGATCA AGTTTCAGCC AGCGATCTTA

GGCACITGGG TTCGGCC

FIG.8A.

AT	ATG	AAA	TCT	GTA	CCT	CTT	ATC	TCT	GGT	GGA	CTT	TCC	TTT	TTA	TTA	1	5	10	15
	Met	Lys	Ser	Val	Pro	Leu	Ile	Ser	Gly	Gly	Leu	Ser	Phe	Leu	Leu				
AGT	GCT	TGT	AGC	GGG	GGA	GGT	GGT	TCT	TTT	GAT	GTA	GAT	GAC	GTC	TCT	20	25	30	
	Ser	Ala	Cys	Ser	Gly	Gly	Gly	Ser	Phe	Asp	Val	Asp	Asp	Val	Ser				
AAT	CCC	TCC	TCT	TCT	AAA	CCA	CGT	TAT	CAA	GAC	GAT	ACT	TCA	AGT	TCA	35	40	45	
	Asn	Pro	Ser	Ser	Lys	Pro	Arg	Tyr	Gln	Asp	Thr	Ser	Ser	Ser	Ser				
AGA	ACA	AAA	TCT	AAA	TTG	GAA	AAT	TTG	TCC	ATT	CCT	TCT	TTA	GCG	GGA	50	55	60	
	Arg	Thr	Lys	Ser	Lys	Leu	Glu	Asn	Leu	Ser	Ile	Pro	Ser	Leu	Gly				
GGG	ATG	AAG	TTA	GIG	GCT	CAG	AAT	CTT	CGT	GAT	AGG	ACA	AAA	CCT	AGT	65	70	75	
	Gly	Met	Lys	Leu	Val	Ala	Gln	Asn	Leu	Arg	Asp	Arg	Thr	Lys	Pro				
CTC	TTA	AAT	GAA	GAT	GAC	TAT	ATG	ATA	TTT	TCC	TCA	CTT	TCA	ACG	ATT	80	85	90	95
	Leu	Leu	Asn	Glu	Asp	Asp	Tyr	Met	Ile	Phe	Ser	Ser	Leu	Ser	Thr				

**FIG.8B.**

AAA GCT GAT GTT GAA AAA GAA AAT AAA CAC TAT ACA AGT CCA GTT GGC	
Lys Ala Asp Val Glu Lys Glu Asn Lys His Tyr Thr Ser Pro Val Gly	110
	100
TCA ATA GAC GAG CCT AGT ACA ACA AAT CCA AAA GAA AAT GAT CAT GGA	
Ser Ile Asp Glu Pro Ser Thr Thr Asn Pro Lys Glu Asn Asp His Gly	125
	115
CAA AGA TAT GTA TAT TCA GGA CTT TAT TAT ATT CCA TCG TGG AAT TTA	
Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp Asn Leu	140
	130
AAC GAT CTT AAA AAT AAC AAG TAT TAT TAT TCT GGT TAC TAT GGA TAT	
Asn Asp Leu Lys Asn Lys Tyr Tyr Tyr Ser Gly Tyr Tyr Gly Tyr	155
	145
GGG TAT TAC TTT GGC AAG CAA ACA GCC ACT ACA TTA CCT GTA AAT GGC	
Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly	175
	160
AAA GTA ACG TAT AAA GGA ACT TGG AGC TTC ATC ACC GCA GCT GAA AAT	
Lys Val Thr Tyr Lys Gly Thr Trp Ser Phe Ile Thr Ala Ala Glu Asn	190
	180
	165
	170
	185

FIG. 8C.

GCC AAA AGG TAT CCT TTG TTA AGT AAT GGC AGT CAA GCT TAT TTT CGA	
Gly Lys Arg Tyr Pro Leu Leu Ser Asn Gly Ser Gln Ala Tyr Phe Arg	195 200 205
CGT AGT GCA ATT CCA GAA GAT ATT GAT TTA GAA GTT AAA AAT GAT GAG	
Arg Ser Ala Ile Pro Glu Asp Ile Asp Leu Glu Val Lys Asn Asp Glu	210 215 220
AAT AGA GAA AAA GGG CTA GTG AGT GAA TTT AGT GCA GAT TTT GGG ACT	
Asn Arg Glu Lys Gly Leu Val Ser Glu Phe Ser Ala Asp Phe Gly Thr	225 230 235
AAA AAA CTG ACA GGA GGA CTG TTT TAC ACC AAA AGA CAA ACT CAT ATT	
Lys Lys Leu Thr Gly Gly Leu Phe Tyr Thr Lys Arg Gln Thr His Ile	240 245 250 255
CAA AAC CAT GAA AAG AAA AAA CTC TAT GAT ATA GAT GCC CAT ATT TAT	
Gln Asn His Glu Lys Lys Lys Leu Tyr Asp Ile Asp Ala His Ile Tyr	260 265 270
AGT AAT AGA TTC AGA GGT AAA GTA AAT CCT ACC CAA AAA GAT TCT AAA	
Ser Asn Arg Phe Arg Gly Lys Val Asn Pro Thr Gln Lys Asp Ser Lys	275 280 285

## FIG.8D.

GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAC GGG  
 Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly  
 290 295 300

CCT GAA GGT CAA GAA TTA GGA GGA AAG TTT TTA GCT GGC GAC AAA AAA  
 Pro Glu Gly Gln Glu Leu Glu Gly Lys Phe Leu Ala Gly Asp Lys Lys  
 305 310 315

GTT TTT GGG GTA TTT AGT GGC AAA GGA ACG GAA AAC AAA AAA TTA  
 Val Phe Gly Val Phe Ser Ala Lys Gly Thr Glu Glu Asn Lys Lys Leu  
 320 325 330 335

CCC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT AAA  
 Pro Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr Lys  
 340 345 350

ACA ACC GAT GCA AAA ACC AAT GCA ACA GCC AAT GCA ACA ACC AGT ACC  
 Thr Thr Asp Ala Lys Thr Asn Ala Thr Ala Asn Ala Thr Thr Ser Thr  
 355 360 365

GCA GCC AAT ACA ACA ACC GAT ACA ACA GCC AAT ACA ATA ACC GAT GCA  
 Ala Ala Asn Thr Thr Thr Asp Thr Thr Ala Asn Thr Ile Thr Asp Ala  
 370 375 380



FIG. 8E.

GAA AAC TTT AAG ACG AAA GAT ATA TCA AGT TTT GGT GAA GCT GAT TAC	
Glu Asn Phe Lys Thr Lys Asp Ile Ser Ser Phe Gly Glu Ala Asp Tyr	
385	390
CTT TTA ATT GAT AAT TAC CCT GTT CCT CTT TTA CCT GAG AGT GGT GAT	
Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Leu Pro Glu Ser Gly Asp	
400	405
TTC ATA AGT AGT AAG CAC CAT ACT GTA GGA AAG AAA ACC TAT CAA GTA	
Phe Ile Ser Ser Lys His His Thr Val Gly Lys Lys Thr Tyr Gln Val	
	410
AAA GCA TGT TGC AGT AAT CTA AGC TAT GTG AAA TTT GGT ATG TAT TAT	
Lys Ala Cys Cys Ser Ser Asn Leu Ser Tyr Val Lys Phe Gly Met Tyr Tyr	
435	440
GAA GTC CCA CCT AAA GAA GAA GAA AAA GAC AAA GAA AAA GAA AAA	
Glu Val Pro Pro Lys Glu Glu Glu Lys Asp Lys Glu Lys Lys Glu Lys	
450	455
GAA AAA GAA AAA CAA CCG ACA AAT CTA TCG AAC ACT TAT TAT CAA TTC	
Glu Lys Glu Lys Lys Gln Ala Thr Asn Leu Ser Asn Thr Tyr Tyr Gln Phe	
465	470

FIG.8F.

TTA TTA GGT CTC CGT ACT CCC AGT TCT GAA ATT CCT AAA GGA GGA AGT	
Leu Leu Gly Leu Arg Thr Pro Ser Ser Glu Ile Pro Lys Gly Gly Ser	
480	495
GCA AAA TAT CTC GGT AGT TGG TTT GGT TAT CTG AGC GAT GGT TCA ACA	
Ala Lys Tyr Leu Gly Ser Trp Phe Gly Tyr Leu Ser Asp Gly Ser Thr	
500	510
TCT TAC TCC CCC AGT GGT GAT AAG AAA CGC GAG AAC AAT GCT CTC GCC	
Ser Tyr Ser Pro Ser Gly Asp Lys Lys Arg Glu Asn Ala Leu Ala	
515	525
GAG TTT AAT GTA AAT TTT GTC GAT AAA ACA TTA AAA GGC CAA TTA ATA	
Glu Phe Asn Val Asn Phe Val Asp Lys Thr Leu Lys Gly Gln Leu Ile	
530	540
CGA CAC GAT AAT CAA AAT ACC GTT TTT ACA ATT GAT GCA ACC TTT AAA	
Arg His Asp Asn Asn Gln Asn Thr Val Phe Thr Ile Asp Ala Thr Phe Lys	
545	555
GGT GGT AAG AAT AAC TTC ACT GGT ACA GCA ACC GCA AAC AAT GTA GCG	
Gly Gly Lys Asn Asn Phe Thr Gly Thr Ala Thr Ala Asn Asn Val Ala	
560	575

**FIG. 86.**

ATT GAT CCC CAA AGT ACA CAA GGC ACA TCT AAC GTC AAT TTC ACG GCA	
Ile Asp Pro Gln Ser Thr Gln Gly Thr Ser Asn Val Asn Phe Thr Ala	580 590
ACA GTA AAT GGG GCA TTT TAT GGG CCG AAC GCT ACA GAA TTA GGC GGT	
Thr Val Asn Gly Ala Phe Tyr Gly Pro Asn Ala Thr Glu Leu Gly Gly	595 600 605
TAT TTC ACC TAT AAC GGA AAT CCT ACA GAT AAA AGT TCC TCA ACC GTA	
Tyr Phe Thr Tyr Asn Gly Asn Pro Thr Asp Lys Ser Ser Thr Val	610 615 620
CCT TCA TCA TCC AAT TCA AAA AAT GCA AGA GCT GCA GTT GTC TTT GGT	
Pro Ser Ser Ser Asn Ser Lys Asn Ala Arg Ala Ala Val Val Phe Gly	625 630 635
GGG AGA CAA CAA GTA GAA ACA ACC AAA TAATGGAATA CTAAAAATGA	
Ala Arg Gln Gln Val Glu Thr Thr Lys	640 645
CTAAAAAAGC TTCTAGAGC CGAATTC	

FIG.9A.

GAATTCGGCT TGGATCCAT ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT	
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu	10
	5
TCC TTT TTA CTA AGT GCT TGT AGC GGA GGG GGT TTT GAT GTA GAT	
Ser Phe Leu Leu Ser Ala Cys Ser Gly Gly Ser Phe Asp Val Asp	25
	20
AAC GTC TCT AAT CCA TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACT	
Asn Val Ser Asn Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr	40
	35
TCA AGT TCA AGA ACA AAA TCT AAT TTG AAA AAG TTG TCC ATT CCT TCT	
Ser Ser Arg Thr Lys Ser Asn Leu Lys Lys Leu Ser Ile Pro Ser	55
	50
TTA GGG GGA GGG ATG AAG TTA GTG GCT CAG AAT CTT AGT GAT AAG AAC	
Leu Gly Gly Met Lys Leu Val Ala Gln Asn Leu Ser Asp Lys Asn	75
	70
AAA CCT AGT CTC TTA AAT GAA GAT GAC TAT ATA TCA TAT TTT TCC TCA	
Lys Pro Ser Leu Leu Asn Glu Asp Tyr Ile Ser Tyr Phe Ser Ser	90
	85

**FIG.9B.**

CTT TCT ACA ATT CAA GAT GAT GTT AAA AAA GAA AAT AAA CGC CAT ACA	
Leu Ser Thr Ile Gln Asp Asp Val Lys Lys Glu Asn Lys Arg His Thr	100
	95
AAT CCA GTT GGC TCA ATA GAC GAG CCT AAC GCA ACA AAT CCA CCC GAA	
Asn Pro Val Gly Ser Ile Asp Glu Pro Asn Ala Thr Asn Pro Pro Glu	110
	115
AAG CAT CAT GGA CAA AGA TAT GTA TAT TCA GGG CTT TAT TAT ATT CCA	
Lys His His Gly Gln Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro	120
	125
TCG TGG AGT CAT TCC TCA AAT GGC AAG CTT TAT TTA GGT TAC TAT GGA	
Ser Trp Ser His Ser Ser Asn Gly Lys Leu Tyr Leu Gly Tyr Tyr Gly	130
	135
TAT GCG TTT TAT TAT GGT AAT AAA ACT GCA ACA AAC TTG CCA GTA AGC	
Tyr Ala Phe Tyr Tyr Gly Asn Lys Thr Ala Thr Asn Leu Pro Val Ser	140
	145
GGC ATA GCT AAA TAC AAA GGA ACT TGG GAT TTT ATT ACT GCA ACT AAA	
Gly Ile Ala Lys Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Lys	150
	155
	160
	165
	170
	175
	180
	185

FIG. 9C.

AAT GGC CAA CGT TAT TCT TTA TTT GGT AGC GCT TTT GGA GCT TAT AAT	
Asn Gly Gln Arg Tyr Ser Leu Phe Gly Ser Ala Phe Gly Ala Tyr Asn	190 195 200
AGA CGC AGT GCT ATT TCA GAA GAT ATA GAT AAT TTA GAA AAT AAT CTA	
Arg Arg Ser Ala Ile Ser Glu Asp Ile Asp Asn Leu Glu Asn Asn Leu	205 210 215
AAG AAT GGT GCG GGA TTA ACT AGT GAA TTT ACT GTC AAT TTT GGT ACG	
Lys Asn Gly Ala Gly Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr	220 225 230 235
AAA AAG CTC ACT GGA AAA CTT TAT TAT AAT GAA AGG GAA ACA AAT CTT	
Lys Lys Leu Thr Gly Lys Lys Leu Tyr Tyr Asn Glu Arg Glu Thr Asn Leu	240 245 250
AAT AAA TTA CAA AAG AGA AAA CAT GAA CTC TAT GAT ATA GAT GCC GAT	
Asn Lys Leu Gln Lys Arg Lys Lys His Glu Leu Tyr Asp Ile Asp Ala Asp	255 260 265
ATT TAT AGT AAT AGA TTC AGA GGT AAA GTA AAG CCA ACA ACC CAA AAA	
Ile Tyr Ser Asn Arg Phe Arg Gly Lys Val Lys Pro Thr Thr Gln Lys	270 275 280

FIG. 9D.

GAT TCT CAA GAA CAT CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT  
 Asp Ser Gln Glu His Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly  
 285 290 295

TTT TAT GGG CCT AAC GGT GAA GAA TTA GGA AAG TTT TTA GCT GGC  
 Phe Tyr Gly Pro Asn Gly Glu Glu Leu Gly Gly Lys Phe Leu Ala Gly  
 300 305 310 315

GAT AAC CGA GTT TTT GGG GTA TTT AGT GCC AAA GAA GAA ACA ACA AAA  
 Asp Asn Arg Val Phe Gly Val Phe Ser Ala Lys Glu Glu Thr Lys  
 320 325 330

GAC AAA AAA TTA TCC AGA GAA ACC TTA ATT GAT GGC AAG CTA ATT ACT  
 Asp Lys Lys Leu Ser Arg Glu Thr Leu Ile Asp Gly Lys Leu Ile Thr  
 335 340 345

TTT AAA AGA ACT GAT GCA ACA ACC AAT ACA GCA GCC AAT GCA AAA ACC  
 Phe Lys Arg Thr Asp Ala Thr Thr Asn Thr Ala Ala Asn Ala Lys Thr  
 350 355 360

GAT GAA AAA AAC TTT ACG ACG AAA GAT ATA CCA AGT TTT GGT GAA GCT  
 Asp Glu Lys Asn Phe Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala  
 365 370 375

FIG.9E.

GAT TAC CTT TTA ATT GAT AAT TAC CCT GTT CCT CTT TTC CCT GAA GAA	
Asp Tyr Leu Leu Ile Asp Asn Tyr Pro Val Pro Leu Phe Pro Glu Glu	395
380	
AAT ACT AAT GAT TTC ATA ACT AGT AGG CAC CAT AAG GTA GGA GAT AAA	
Asn Thr Asn Asp Phe Ile Thr Ser Arg His His Lys Val Gly Asp Lys	410
400	
ACC TAT AAA GTA GAA GCA TGT TGC AAG AAT CTA AGC TAT GTG AAA TTT	
Thr Tyr Lys Val Glu Ala Cys Cys Lys Asn Leu Ser Tyr Val Lys Phe	425
415	
GGT ATG TAT TAT GAA GAC CCA TTA AAT GGA GAA AAT GGC AAA GAA AAA	
Gly Met Tyr Tyr Glu Asp Pro Leu Asn Gly Glu Asn Gly Lys Glu Lys	440
430	
GAA AAA GAA AAA GAA AAA GAC AAA GAA AAA CAA CCG ACA ACA TCT ATC	
Glu Lys Glu Lys Glu Lys Asp Lys Glu Lys Gln Ala Thr Thr Ser Ile	455
445	
AAG ACT TAT TAT CAA TTC TTA TTA GGT CAC CGT ACT GCC AAG GCC GAC	
Lys Thr Tyr Tyr Gln Phe Leu Leu Gly His Arg Thr Ala Lys Ala Asp	475
460	



FIG.9F.

ATA CCT GCA ACG GGA AAC GTG AAA TAT CGC GGT AAT TGG TTT GGT TAT	
Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly Asn Trp Phe Gly Tyr	480 485 490
ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT GGA GAT AAA AAT GCT	
Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr Gly Asp Lys Asn Ala	495 500 505
GTC GCC GAG TTT GAT GTA AAT TTT GCC GAT AAA ACA TTA ACA GGC ACA	
Val Ala Glu Phe Asp Val Asn Phe Ala Asp Lys Thr Leu Thr Gly Thr	510 515 520
TTA AAA CGA CAC GAT AAT GGA AAT CCC GTA TTT ACA ATT AAT GCA AGC	
Leu Lys Arg His Asp Asn Gly Asn Pro Val Phe Thr Ile Asn Ala Ser	525 530 535
TTT CAA AGT GGT AAG AAT GAC TTC ACT GGT ACA GCA ACC GCA AAC AAT	
Phe Gln Ser Gly Lys Asn Asp Phe Thr Gly Thr Ala Thr Ala Asn Asn	540 545 550 555
GTA GCG ATT GAT CCC CAA AAT ACA CAA ACC ACA TCT AGA GTC AAT TTC	
Val Ala Ile Asp Pro Gln Asn Thr Gln Thr Thr Ser Arg Val Asn Phe	560 565 570

# FIG.96.

ACG GCA ACA GTA AAC GGG GCA TTT TAT GGA CCT AAG GCT ACA GAA TTA  
 Thr Ala Thr Val Asn Gly Ala Phe Tyr Gly Pro Lys Ala Thr Glu Leu  
 575 580 585

GGC GGT TAT TTC ACT TAT AAC GGA AAC AAT CCT ACA GAT AAA AAT TCC  
 Gly Gly Tyr Phe Thr Tyr Asn Gly Asn Asn Pro Thr Asp Lys Asn Ser  
 590 595 600

TCA ACC GTT TCA CCA TCC AAT TCA GCA AAT GCT CGT GCT GCC GTT GIG  
 Ser Thr Val Ser Pro Ser Asn Ser Ala Asn Ala Arg Ala Ala Val Val  
 605 610 615

TTT GGC GCT AAA AAA CAA GTA GAA ACA ACC AAC AAG TAAAAACAAC  
 Phe Gly Ala Lys Lys Gln Val Glu Thr Thr Asn Lys  
 620 625 630

CAAGTAATGG AATACTAAAA ATGACTAAAA AAGCTTCTAG AAAGCCGAAT TC

FIG.10A.

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC CTT TTA TTA AGT	
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Leu Leu Ser	15
1 5 10	
GCT TGT AGC GGG GGA GGT GGT TCT TTT GAT GTA GAT GAC GTC TCT AAT	
Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asp Val Ser Asn	30
20 25	
CCC TCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AGT CAA AGA	
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Ser Gln Arg	45
35 40	
ACA AAA TCT AAT TTG GAA AAG TTG TCC ATT CCT TCT TTA GGA GGA GGG	
Thr Lys Ser Asn Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Gly	60
50 55	
ATG AAA TTG GTG GCT CAG AAT CTG AGT AGT GGT AAT AAA GAA CCT AGT TTC	
Met Lys Leu Val Ala Gln Asn Leu Ser Gly Asn Lys Glu Pro Ser Phe	80
65 70 75	
TTA AAT GGA AAT GAC TAT ATG ATA TTT TCC TCA CGT TCT ACG ATT AAA	
Leu Asn Gly Asn Asp Tyr Met Ile Phe Ser Ser Arg Ser Thr Ile Lys	95
85 90	

FIG.10B.

GAT GAT GTT GAA AAT AAC AAT ACA AAC GGG GGG GAC TAT ATT GGC TCA	
Asp Asp Val Glu Asn Asn Asn Thr Asn Gly Gly Asp Tyr Ile Gly Ser	100 105 110
ATA GAC GAG CCT AGT ACA ACA AAT CCA CTC GAA AAG CAT CAT GGA CAA	
Ile Asp Glu Pro Ser Thr Thr Asn Pro Leu Glu Lys His His Gly Gln	115 120 125
AGG TAT GTA TAT TCA GGG CTT TAT TAT ATT CAA TCG TGG AGT CTA AGA	
Arg Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Gln Ser Trp Ser Leu Arg	130 135 140
GAT TTA CCA AAG AAG TTT TAT TAT TCA GGT TAC TAT GGA TAT GCG TAT TAC	
Asp Leu Pro Lys Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr Ala Tyr Tyr	145 150 155 160
TTT GGC AAG GAA ACA GCC ACT ACA TTA CCT GTA AAT GGC GAA GCA ACG	
Phe Gly Lys Glu Thr Ala Thr Thr Leu Pro Val Asn Gly Glu Ala Thr	165 170 175
TAT AAA GGA ACT TGG GAT TTC GAT TTC ATC ACT GCA ACT AGA AAT GGC AAA AGT	
Tyr Lys Gly Thr Trp Asp Phe Ile Thr Ala Thr Arg Asn Gly Lys Ser	180 185 190

FIG.10C.

TAT TCT TTG TTA AGT AAT AAC CGA CAA GCT TAT TCC AAA CGT AGT GCA	
Tyr Ser Leu Leu Ser Asn Asn Arg Gln Ala Tyr Ser Lys Arg Ser Ala	205
	195 200
ATT CCA GAA GAC ATT GAT TTA GAA AAT GAT CCA AAG AAT GGT GAG ACG	
Ile Pro Glu Asp Ile Asp Leu Glu Asn Asp Pro Lys Asn Gly Glu Thr	220
	210 215
AGA TTA ACT AGT GAA TTT ACT GTG AAT TTT GGT ACG AAA AAG CTC ACA	
Arg Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr	240
	225 230 235
GGT GGA CTT TAT TAC CAT TTA CGT AAA ACA AAT GCT AAT GAA AAC CAA	
Gly Gly Leu Tyr Tyr His Leu Arg Lys Thr Asn Ala Asn Glu Asn Gln	255
	245 250
AAT AGA AAA CAT AAA CTC TAC AAT CTA GAA GCT GAT GTG TAT AGC AAC	
Asn Arg Lys His Lys Leu Tyr Tyr Asn Leu Glu Ala Asp Val Tyr Ser Asn	270
	260 265
CGA TTC AGA GGT AAA GTA AAG CCA ACC AAA GAG TCT TCT GAA GAA CAT	
Arg Phe Arg Gly Lys Val Lys Pro Thr Lys Glu Ser Ser Glu Glu His	285
	275 280

FIG.10D.

```

CCC TTT ACC ACC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT
Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Gly Phe Tyr Gly Pro Asn
290                                     295 300

GCT GAA GAA CTA GGG GGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT
Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe
305                                     310 315 320

GGG GTA TTT AGT GCC AAA GAA GAA CAG CAA GAA ACG GAA AAC AAA AAA
Gly Val Phe Ser Ala Lys Glu Glu Gln Gln Thr Glu Glu Asn Lys Lys
325                                     330 335

TTA CTC AAA GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT ACT
Leu Leu Lys Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Thr
340                                     345 350

AAA AAA ACC AAT GCA ACA ACC GAT GCA ACA ACC AGT ACA ACC AGT
Lys Lys Thr Asn Ala Thr Thr Asp Ala Thr Thr Ser Thr Thr Ser
355                                     360 365

ACA GCA ACC AAT GCA ACA GCC GAT GCA GAA AAC TTT ACG ACA AAA GAT
Thr Ala Thr Asn Ala Thr Ala Asp Ala Glu Asn Phe Thr Thr Lys Asp
370                                     375 380

```

FIG.10E.

ATA TCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT GAT AAT TAC CCT	
Ile Ser Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile Asp Asn Tyr Pro	385 390 395 400
GTT CCT CTT TTA CCT GAA AAT ACT AAT GAT TTC ATA AGC AGT AAG CAC	
Val Pro Leu Leu Pro Glu Pro Glu Asn Thr Asn Asp Phe Ile Ser Ser Lys His	405 410 415
CAT GAG GTA GGA GGT AAA CAC TAT AAA GTG GAA GCA TGT TGC AAG AAT	
His Glu Val Gly Gly Lys His Tyr Lys Val Glu Ala Cys Cys Lys Asn	420 425 430
CTA AGC TAT GTG AAA TTT GGT ATA TAT TAT GAG GAT AAT GAG AAG AAC	
Leu Ser Tyr Val Lys Phe Gly Ile Tyr Tyr Glu Asp Asn Glu Lys Asn	435 440 445
ACC AAA ATT GAA ACA GAA CAA TAC CAC CAA TTT TTG TTA GGT CTC CGT	
Thr Lys Ile Glu Thr Glu Gln Tyr His Gln Phe Leu Leu Gly Leu Arg	450 455 460
ACT CCC AGT TCT CAA ATT CCT GCA ACG GGA AAC GTG AAA TAT CGC GGT	
Thr Pro Ser Ser Gln Ile Pro Ala Thr Gly Asn Val Lys Tyr Arg Gly	465 470 475 480

FIG.10F.

AGT TCG TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC ACT ACT  
 Ser Trp Phe Gly Tyr Ile Gly Asp Asp Lys Thr Ser Tyr Ser Thr Thr  
 485 490  
  
 GGA GAT AAA AAT GCT CTC GCC GAG TTT GAT GTA AAT TTT ACC GAT AAA  
 Gly Asp Lys Asn Ala Leu Ala Glu Phe Asp Val Asn Phe Thr Asp Lys  
 500 505 510  
  
 AAG CTA ACA GCG GAA TTA AAA CGA GCC GAT AAT CAA AAT ACC GTA TTT  
 Lys Leu Thr Gly Glu Leu Lys Arg Ala Asp Asn Gln Asn Thr Val Phe  
 515 520 525  
  
 AGA ATT AAT GCA GAC TTT AAA AAT AAT GAT AAT GCC TTC AAA GGT ACA  
 Arg Ile Asn Ala Asp Phe Lys Asn Asn Asp Asn Ala Phe Lys Gly Thr  
 530 535 540  
  
 GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAC AAT AGT CAA ACT GGA  
 Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Asn Asn Ser Gln Thr Gly  
 545 550 555 560  
  
 AAT ACC CAA ATT AAT ATT AAA ACT GAA GTA AAT GGG GCA TTT TAT GGT  
 Asn Thr Gln Ile Asn Ile Lys Thr Glu Val Asn Gly Ala Phe Tyr Gly  
 565 570 575



# FIG.10G.

CCG AAC GCT ACA GAA TTA GGC GGT TAT TTC ACT TAT AAC GGA AAA AAT  
 Pro Asn Ala Thr Glu Leu Gly Gly Tyr Phe Thr Tyr Asn Gly Lys Asn  
 580 585 590

CCT ACA GAT AAA AAT TCT GAA AGT TCC TCA ACC GTA CCT TCA CCA CCC  
 Pro Thr Asp Lys Asn Ser Glu Ser Ser Thr Val Pro Ser Pro Pro  
 595 600 605

AAT TCA CCA AAT GCA AGA CCT GCA GTT GTC TTT GGT GCT AAA AAA CAA  
 Asn Ser Pro Asn Ala Arg Ala Ala Val Val Phe Gly Ala Lys Lys Gln  
 610 615 620

GTA GAA AAA AAC AAC AAG TAAACAAC CAAGTAATGG AATACTAAAA  
 Val Glu Lys Asn Asn Lys  
 625 630

ATGACTAAAA AAGCTTCTAG AAGCCGAAT C

**FIG.11A.**

ATG AAA TCT GTA CCT CTT ATC TCT GGT GGA CTT TCC TTT TTA CTA AGT	
Met Lys Ser Val Pro Leu Ile Ser Gly Gly Leu Ser Phe Leu Leu Ser	
1 5 10 15	
GCT TGT AGC GGA GGG GGG TCT TTT GAT GTA GAT AAC GTC TCT AAT ACC	
Ala Cys Ser Gly Gly Gly Ser Phe Asp Val Asp Asn Val Ser Asn Thr	
20 25 30	
CCC TCT TCT AAA CCA CGT TAT CAA GAC GAT ACC TCG AAT CAA AGA ACA	
Pro Ser Ser Lys Pro Arg Tyr Gln Asp Asp Thr Ser Asn Gln Arg Thr	
35 40 45	
AAA TCT AAA TTG GAA AAG TTG TCC ATT CCT TCT TTA GGA GGA GGG ATG	
Lys Ser Lys Leu Glu Lys Leu Ser Ile Pro Ser Leu Gly Gly Met	
50 55 60	
AAG TTA GTT GTG CAA AAT TTT GCT GGT GCT AAA GAA CCT AGT TTC TTA	
Lys Leu Val Val Gln Asn Phe Ala Gly Ala Lys Glu Pro Ser Phe Leu	
65 70 75 80	
AAT GAA AAT GAC TAT ATA TCA TAT TTT TCC TCA CTT TCT ATG ATT AAA	
Asn Glu Asn Asp Tyr Ile Ser Tyr Phe Ser Ser Leu Ser Met Ile Lys	
85 90 95	

FIG.11B.

GAT GAT GTT GAA AAT AAC AAT AAA AAT AAG GAT ACT CCA ATT GGC TCA	
Asp Asp Val Glu Asn Asn Lys Asn Lys Asp Thr Pro Ile Gly Ser	100 110
ATA GAC GAG CCT AGA GCA CCA AAT TCA AAC GAA AAT CAT CAA AAT CAT	
Ile Asp Glu Pro Arg Ala Pro Asn Ser Asn Glu Asn His Gln Asn His	115 120 125
CAT GGA CAG CAA TAT GTA TAT TCG GGT CTT TAT TAT ATT CCA TCG TGG	
His Gly Gln Gln Tyr Val Tyr Ser Gly Leu Tyr Tyr Ile Pro Ser Trp	130 135 140
CGT CTA ATA AAT TTA CCA AAT AAG TTT TAT TCA GGT TAC TAT GGA TAT	
Arg Leu Ile Asn Leu Pro Asn Lys Phe Tyr Ser Gly Tyr Tyr Gly Tyr	145 150 155 160
GCG TAT TAC TTT GGC AAG CAA ACT GCC ACT ACA TTA CCT GTA AAT GGC	
Ala Tyr Tyr Phe Gly Lys Gln Thr Ala Thr Thr Leu Pro Val Asn Gly	165 170 175
GAA GCA ACG TAT AAA GGA ACT TGG AGC TTC ACC GCA ACT GAA AGA	
Glu Ala Thr Tyr Lys Lys Gly Thr Trp Ser Phe Ile Thr Ala Thr Glu Arg	180 185 190

FIG.11C.

GGC AAA AAT TAT TCT TTG TTC AAT AAT AGA GGT CAA GCT TAT TCT CGA	
Gly Lys Asn Tyr Ser Leu Phe Asn Asn Arg Gly Gln Ala Tyr Ser Arg	195 200 205
CGT AGT GCT ACT CCA GGA GAT ATT GAT TTA GAA AAC GGT GAC GCA GGC	
Arg Ser Ala Thr Pro Gly Asp Ile Asp Leu Glu Asn Gly Asp Ala Gly	210 215 220
TTA ACA AGT GAA TTT ACT GTC AAT TTT GGT ACA AAA AAG CTC ACT CGA	
Leu Thr Ser Glu Phe Thr Val Asn Phe Gly Thr Lys Lys Leu Thr Gly	225 230 235 240
GAA CCT TAT TAT AAT GAA AGG GAA ACA AAT CTT AAT CAA TCA AAA GAT	
Glu Pro Tyr Tyr Asn Glu Arg Glu Thr Asn Leu Asn Gln Ser Lys Asp	245 250 255
AGA AAA CAT AAA CTC TAC GAT CTA GAA GCT GAT GTG TAT AGC AAC CGA	
Arg Lys His Lys Leu Tyr Asp Leu Glu Ala Asp Val Tyr Ser Asn Arg	260 265 270
TTT AGA GGT ACA GTA AAG CCA ACC AAA AAA GAG TCT TCT GAA GAA CAT	
Phe Arg Gly Thr Val Lys Pro Thr Lys Lys Glu Ser Ser Glu Glu His	275 280 285

FIG.11D.

CCC TTT ACC AGC GAG GGA ACA TTA GAA GGT GGT TTT TAT GGG CCT AAT  
 Pro Phe Thr Ser Glu Gly Thr Leu Glu Gly Phe Tyr Gly Pro Asn  
 290 295 300  
  
 GCT GAA GAA CTA GGG GGA AAA TTT TTA GCT AGC GAT AAA AAA GTT TTT  
 Ala Glu Glu Leu Gly Gly Lys Phe Leu Ala Ser Asp Lys Lys Val Phe  
 305 310 315 320  
  
 GGG GTA TTT AGT GCC AAA GAA ACG GAA GAA CCA AAA TTA CCC AAA  
 Gly Val Phe Ser Ala Lys Glu Thr Glu Glu Lys Pro Lys Leu Pro Lys  
 325 330 335  
  
 GAA ACC TTA ATT GAT GGC AAG CTA ACT ACT TTC TCT AAA ACA ACC GAT  
 Glu Thr Leu Ile Asp Gly Lys Leu Thr Thr Phe Ser Lys Thr Thr Asp  
 340 345 350  
  
 ACA ACA ACC AAT AAA ACA ACC AGT GCA AAA ACC AAT ACA GAA AAC TTT  
 Thr Thr Thr Asn Lys Lys Thr Ser Ala Lys Thr Asn Thr Glu Asn Phe  
 355 360 365  
  
 ACG ACA AAA GAT ATA CCA AGT TTT GGT GAA GCT GAT TAT CTT TTA ATT  
 Thr Thr Lys Asp Ile Pro Ser Phe Gly Glu Ala Asp Tyr Leu Leu Ile  
 370 375 380

FIG.11E.

GAT AAT TAC CCT ATT CCG CTT TTA CCT GAG AGT GGT GAT TTC ATA AGT	
Asp Asn Tyr Pro Ile Pro Leu Leu Pro Glu Ser Gly Asp Phe Ile Ser	
385	390 395 400
AGT AAG CAC CAT GAG GTA GGA GGT AAA CGC TAT AAA GTG GAA GCA TGT	
Ser Lys His Glu Val Gly Gly Lys Arg Tyr Lys Val Glu Ala Cys	
405	410 415
TGC AAG AAT CTA TGC TAT GTG AAA TTT GGT ATG TAT TAT GAG GAT AAA	
Cys Lys Asn Leu Cys Tyr Val Lys Phe Gly Met Tyr Tyr Glu Asp Lys	
420	425 430
GAG AAC AAC AAA AAT GAA ACA GAC AAA GAA AAA GAA CAA ACG ACA	
Glu Asn Asn Lys Asn Glu Thr Asp Lys Glu Lys Glu Lys Gln Thr Thr	
435	440 445
ACA TCT ATC AAG ACT TAT TAT CAA TTC TTA TTA GGT CTC CGG ACT CCC	
Thr Ser Ile Lys Thr Tyr Tyr Gln Phe Leu Leu Gly Leu Arg Thr Pro	
450	455 460
AGT TCT GAA ATT CCT AAA ATG GGA AAC GTG ACA TAT CGC GGT AGT TGG	
Ser Ser Glu Ile Pro Lys Met Gly Asn Val Thr Tyr Arg Gly Ser Trp	
465	470 475 480

FIG.11F.

TTT GGT TAT ATT GGT GAT GAC AAG ACA TCT TAC TCC GCT ACA GGA GAT	
Phe Gly Tyr Ile Gly Asp Lys Thr Ser Tyr Ser Ala Thr Gly Asp	485 490 495
AAA CGA CAA GAT AAA AAT GCT CCC GCC GAG TTT AAT GCT GAT TTT AAC	
Lys Arg Gln Asp Lys Asn Ala Pro Ala Glu Phe Asn Ala Asp Phe Asn	500 505 510
AAT AAA AAG CTA ACA GGC ACA TCA AAA CGA CAC GAT AAT CAA AAT CCC	
Asn Lys Lys Leu Thr Gly Thr Ser Lys Arg His Asp Asn Gln Asn Pro	515 520 525
GTG TTT AAC ATT AAG GCA ACC TTT CAA AAT GGT CCG AAT GAC TTT GAA	
Val Phe Asn Ile Lys Ala Thr Phe Gln Asn Gly Arg Asn Asp Phe Glu	530 535 540
GGT ACA GCA ACC GCA GAA AAT TTT GTA ATA GAT GGT AAA GAT AGT CAA	
Gly Thr Ala Thr Ala Glu Asn Phe Val Ile Asp Gly Lys Asp Ser Gln	545 550 555 560
GGA AAT ACC CCA ATT AAT ATT ACA ACT AAA GTA AAC GGG GCA TTT TAT	
Gly Asn Thr Pro Ile Asn Ile Thr Thr Lys Val Asn Gly Ala Phe Tyr	565 570 575

# FIG.11G.

GGA CCT GAT GCT TCT GAA TTA GGC GGT TAT TTC ACC TAT AAC GGA AAA  
 Gly Pro Asp Ala Ser Glu Leu Gly Tyr Phe Thr Tyr Asn Gly Lys  
 580 585 590

GAC ACT ATA ACT AAA AAT ACT GAA AGT TCC TCA ACC GTA CCT TCA CCA  
 Asp Thr Ile Thr Lys Asn Thr Glu Ser Ser Thr Val Pro Ser Pro  
 595 600 605

CCC AAT TCA CCA AAT GCA AGA GCT GCA GTT GIG TTT GGA GCT AAA AAA  
 Pro Asn Ser Pro Asn Ala Arg Ala Ala Val Phe Gly Ala Lys Lys  
 610 615 620

CAA GTA GAA ACA ACC AAC AAG TAGAAAAAA CAAATAATCG AATACTAAAA  
 Gln Val Glu Thr Thr Asn Lys  
 625 630

ATGACTAAAA AAGCTTCTAG AAAGCCGAAT TC



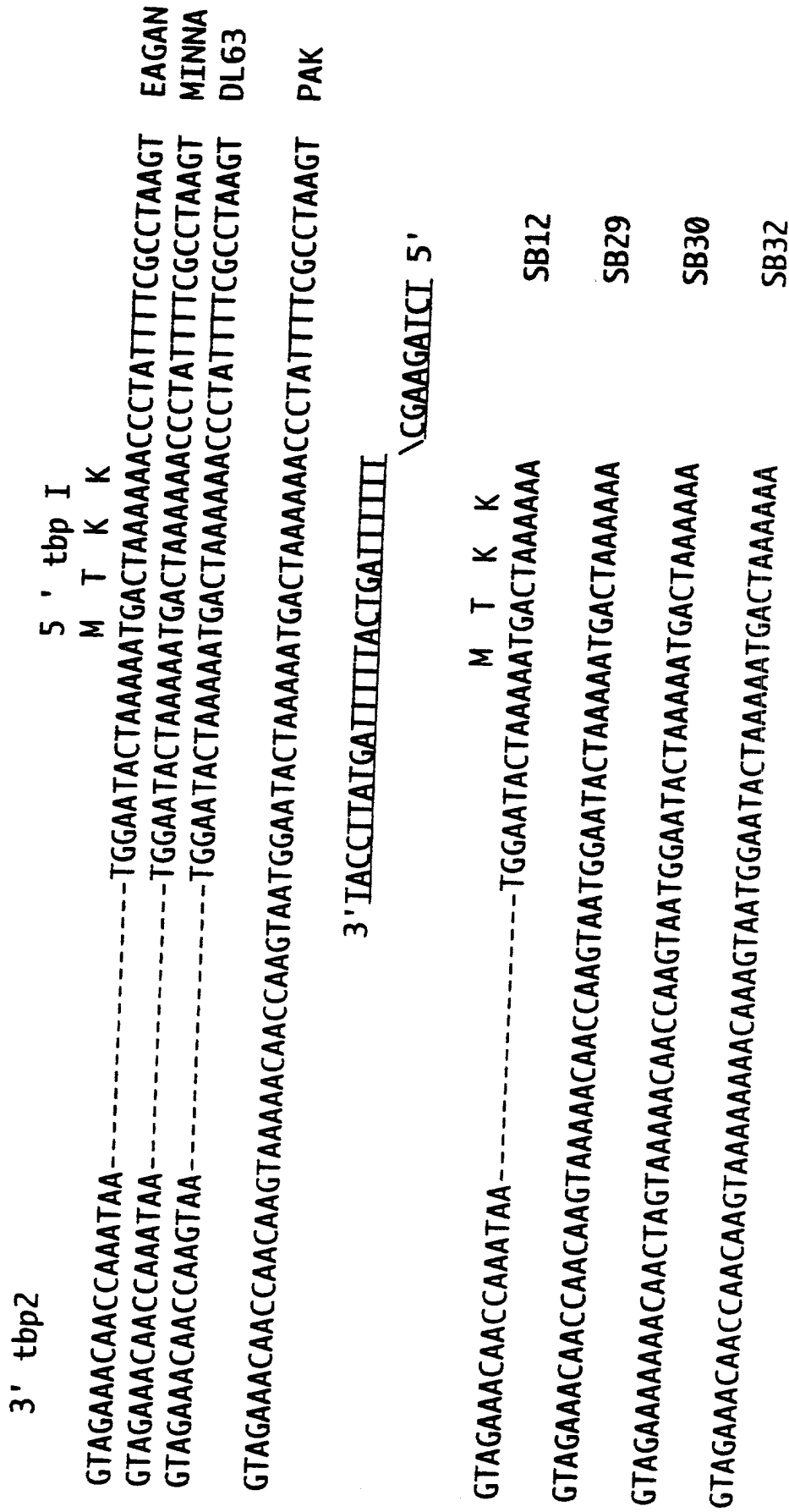
**FIG. 12A**

[illegible]

...5'GGATCCAT  
... \ATGAAATCTGTACCTCTTATCTCTGGT 3'

...                M    K    S    V    P    L    I    S    G  
...TATATAATTCTATGAAATCTGTACCTCTTATCTCTGGT          EAGAN  
...TATATAATTCTATGAAATCTGTACCTCTTATCTCTCGT          MINNA  
...TAT-TAATTCTATGAAATCTGTACCTCTTATCTCTCGT          PAK  
...AATATAATTCTATGAAATCTGTACCTCTTATCTCTCGT          SB33

FIG.12B



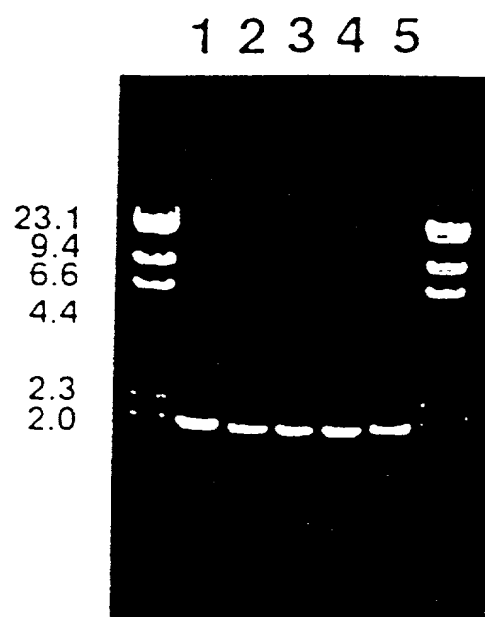


FIG.13.

FIG.14 A.

Comparison of TBP1 amino acid sequences

MTKKPYFRLSIISCLLISCVVKAETQSIKDTKEAISSEVDTSQSTEDSELETISVTAEKIRDRKNEVTGLGKIIKTSESISREQVLNIRDLTRYPGISV	EAGAN
.....V.....	DL63
.....	PAK
.....	SB33
.QQQHL...N.L...SLMTALPVYAENTQAEQAQEKQ-----D..Q.K.K.QKT.R.....LV.S.DTL.K.....A.	B16B
.QQQHL...N.L...SLMTALP.YAENTQAGQAQEKQ-----D..Q.K.K.QKT.R.....LV..ADTL.K.....D.....A.	M982
.QQQHL...N.L...SLMTALP.YAENTQAGQAQEKQ-----D..Q.K.K.QKT.R.....LV..ADTL.K.....D.....A.	FA19
VEQGRGASSGYSIRGMDNRNVALVDGLPQTQSYVVQSPPLVARSGYSGTGAINIEYENVKAVEISKGSSESSEYGNALAGSVTFQSKSAADILEGDKSW	EAGAN
.....	DL63
.....	PAK
.....	SB33
.....K...S.T...VS.I...TA.AA.GGTRTAGSS.....SN.....A..T.T...IGEG.Q.	B16B6
.....K...S.T...A.I...TA.AA.GGTRTAGSS.....SN.V.Q.S.....A..T.T.D.VIGEGRQ.	M982
.....K...S.T...A.I...TA.AA.GGTRTAGSS.....SN.V.Q.S.....A..T.T.D.VIGEGRQ.	FA19
GIQTKNAYSSKNKGFTSLAVAGKQGGFEGLAIYTQRNSIETQVHKDALKGVSQSYDRLLIATTDKSSGYFVIQG-----ECPNGDDK--CAA--KPPATLS	EAGAN
.....V...H.....F...EDQ.A...M.D-----LD.Y.--KTSP.R.....	DL63
.....D.V.....H...KPEDQ.A...M.D-----KP..YNS.LPFA.R..I..	PAK
.....V.....E.F.....E.F.....KV.	SB33
...S.T...G.DHAL.Q...L..RS..A.A.L...K.RGR.IHA...G...FN..VLDE..KE.GSQRYRFIVEE..H..YAA--..KNKL.ED.SVK	B16B6
...S.T...G..R.L.Q.I.L..RI..A.A.L.H.K.RGG.IRA.E..GR...FN..VLVE.----SSEYAYFIVED..EGKNYET-.KSKP.KDVVGK	M982
...S.T...G..R.L.Q.I.L..RI..A.A.L.H.K.RGG.IRA.EA.GR...FN..APVD.----GSKYAYFIVEE..K..GHEK-.K.NP.KDVVGE	FA19

FIG.14B.

TQSETVSVSDYTGANRIKPNPKYESQSWFLRGYHFSE-QHYIGGIFEFTQQKFDIRDMTFPAYLSPTERRDDSSRSFYPMQDHGAYQHIEDGR-----	EAGAN
..R.....R...DK.LQ..P..K..Y.....G.....	DL63
S.R.....RS.K.....G.....K..Y.....R.....	PAK
P.....RS.K.....RTGP...K..Y.....R.....	SB33
DERK...TQ...S..LLA..LE.G...LF.P.W.LDN-R..V..AVL.R...T..T...V...FTSEDYVP-----GSLKGLGKYSKGNKAE.LFVQG	B16B6
DERQ...TR...P..FLAD.LS...R..LF.P.FR.ENKRR...L.H...T..T...V..F.TKAVFDAN.KQAGSLPGNKGYAGNHKY.GLFTNG	M982
DERQ...TR...P..FLAD.LS...R..LF.P.FR.ENKRR...L.H...T..T...V..F.TKAVFDANQKQAGSLPGNKGYAGNHKY.GLFTSG	FA19
-----GVKYASGLYFDEHHRKQRVGIEYIYENKNKAGIIDKAVLSANQQNIILDSYMRHTHCSLYPNPSKNCRPTLDKPYSYRSDRNVYKEKHMLQL	EAGAN
-----N.....H.....	DL63
-----N.....R.....H.....	PAK
-----N.....Q.....R.....H.....	SB33
EGSTLQ.IG.GT.VFY..R.T.N.Y.V..V.H.AD.DTWA.Y.R..YDR.G.D..NRLQQ...HDGSD-...DGN...F.K...MI.E.SR.LF.A	B16B6
ENGALV.AE.GT.VFY..T.T.S.Y.L..V.T.AD.DTWA.Y.R..YDR.G.D..NHFQQ...ADGSD-..Y..SA...F...K...VI.G.S.RL..A	M982
ENNAVP.AE.GT.VFY..T.T.S.Y.L..V.T.AD.DTWA.Y.R..YDR.G.D..NHFQQ...ADG-..Y..SA...F...K...VI.G.S.KL..A	FA19
NLEKKIQQNWLTHQIVFNLGFDDFTSALQHKDYLTRRVIATADSIPRKPGETGKPRNGLQSQ-PYLYPKPEPYFAGQDHCNYQGSSSNYRDCVKRLIKGK	EAGAN
.....A.....S..SE.R..A--R.....S-.....T.KAELV.G.L.....K...S.....	DL63
.....T..K..SE.AN.--R...YKK.-...TVG.VV...D.K.N.....	PAK
.....T...NI.SGTVA--R...YEK.-...S.KVG.V.....K.....S.....	SB33
VFK.AFDTAKIR.NLSI...Y.R.K.Q.S.S..YLQNAVQAY.L.TP.KPPFP---.SKDN-..RVSIGKTTVNTSPI.RFGNNT--Y..TP.N.G.N	B16B6
AFK.SFDTAKIR.NLSV...R.D.N.R.Q..YYQHANRAYS.KTPPKTANP---.DK.K-..WVSIGCGNVVTGQI.LFGNNT--Y..TP.S.N..	M982
AFK.SFDTAKIR.NLSV...Y.R.G.N.R.Q..YYQSANRAYS.LKTPPONNGK.TSPNGREKN..WVSIGRGNVVTRQI.LFGNNT--Y..TP.S.N..	FA19
NYFYAARNMALGKYVDLGLGIRYDVSRRTKANESTISVGKFKNFSWNTGIVIKPTIEWLDSLRLSTGFRNPSFSEMYGWRYGKNDDEVYVGKFKPETS RN	EAGAN
.....M.....A.....DTD..I.....	DL63
.....A.....N.S.....	PAK

FIG.14C.

.....I.....	.....A.....	.....N.SD.....	SB33
G..A.VQD.VR..RWA.V.A....YRS.HSEKSV.T.THR.L...A.V.L..FT.M.T.A...L..A...A.---ESLKTLDL...K.F.			B16B6
G..A.V.D.VR..RWA.V.A.L...YRS.HSDDGSV.T.THRTL...A..L..AD...T.A...L..A...S.---VQSKAV.ID..K.F.			M982
S..A.V.D.VR..RWA.V.A.L...YRS.HSDDGSV.T.THRTL...A..L..AD...T.A...L..A...S.---KIKAV.ID..K.F.			FA19
QEFGLALKGDFGNIEISHFSNAYRNLIATAFAEELSKNG-TGKGNV--GYHNAQNAKLGVGNITAQLDFNGLWKRIPIYGYWATFAYNQVKVDQKINAGLAS			EAGAN
.....T.....	.....R.....		DL63
.....N..-..A..-..	.....R.....		PAK
.....T.....	.....R.....		SB33
R.A.IVF.....L.A.Y.N...D...GY.TRTQNGQTSASGDP..R...RIA.I..LGKI.WH.V.GGL.D.L.S.L..RI...AD.R.DRTF			B16B6
K.A.IVF.....L.A.W.N...D..VRGY.AQIKNGKEEAKGDDPA.L...S.RIT.I..LGKI.W..V.DKL.E..S...R.H.R.I.KR.DRTD			M982
K.A.IVF.....L.A.W.N...D..VRGY.AQIKDGKEQVKGNPA.L...S.RIT.I..LGKI.W..V.DKL.E..S...R.R.R.I.KR.DRTD			FA19
VSSYLFDAIQPSRYIIGLYDHPSTWGINWFTQSKAKSQNELLGKRALGNNSRD-VKSTRKLTRAWHILDVSGYMANKNIMLRGLIYNLFNRYVTW			EAGAN
.....K.....	.....V.RS.LF...V..L.....		DL63
.....N-.....			PAK
.....Q.....N-.....			SB33
.T.....V.....VL.....DGI.....Y.....VD...SQ..L.GNANAK.AASRR..P.YVT...NIK.HLT..A.V..L...			B16B6
IQ.H.....VW.....Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V...TIK.HFT..A.V..L.....			M982
IQ.H.....VW.S...Q.EGK..V.G.L.Y...EIT...S...L.GNSRNT.A.ARR..P.Y.V...TVK.HFT..A.V..L.H.....			FA19
EAVRQTAQGAVNQHNVGSYTRYAASGRNYTLTLEMKF*	EAGAN		
.....N.....*	DL63		
.....*	PAK		
.....*	SB33		
N.....G.....K...V.N...P....FS.....*	B16B6		
N.....G.....G.K...V.N...P....FS.....*	M982		
N.....A.....K...V.N...P....FS.....*	FA19		

FIG.15A.

Comparison of TNP2 amino acid sequences

MKSVPLISGGLSACSGG-SFDVDNVSNTPS--SKPRYQDDTS---NQRKKS-NLKKLFIPSLGGMKLVAQNLRGNREPSFLNEDDIYSYFSS	EAGAN
.....G.....D.....PS.....T.....K.E.S.....A.L..FDRNK..L.....S.M-I...	DL63
.....G.....D.....PS.....T.....D.E.....FI.AR.....G.M-I...	PAK
.....G.....D.....PS.....SS.T.-K.EN.S.....DRTK..L.....M-I...	SB12
.....G.....D.....PS.....SS.T.-.....S.....FDRNK..L.....	SB19
.....L.....D.....PS.....S.T.-E..S.....S.....GN..M-I...	SB30
.....T.-K.E.S.....V..FA.A.....N.....	SB32
MNPLVNQAAMVLPV.....L..G..L.S.ETVODMH...K.E.EK.Q-PES.QDV.E.SGAAYGFAVKLPRRNAHF.PKYKFKHKP.GSM.WKKLO-R	B16B6
MNPLVNQAAMVLPV.....L..G..L.S.DT-EAPRPA.K...VS.EKPQA.KD---QG-GYGFAMRLKRRN--WYPGAESEVK...S.WEATGLP	M982
MNPLVNQAAMVLPV.....L..G..L.S.DT-EAPRPA.K...VP.KKPEARKD---QG-GYGFAMRFKRRNQHPSPANKEDEVK.KN..WEATGLP	FA19
MHFKNLPYALAFSL..-V.....KG...LED.RPNKTTGVSKEEYK.VETAKKEQ-----GE.ME.A..YVV.V-----VSSF.NKKVDI---	AP205
MHFKNLPYALAFSL..-V.....KG...LED.RPNQTAKEKATTSYQDEETKKKT.--EE.D..ME.A..YET---I..R..A.KTETGEKRNREV--	AP37
L-----STIEKDVK---DNMKNAGADLIGSIDEPTNPPEK---HHGQF-----YVYSGLYYTPSWSLNDSKN-KF-----YLGYYGYAFY	EAGAN
R-----E...--ND.Q..EHP.D..VD.RAP.SN.N---R.....IQ....R.LP.K.-----S.....Y.	DL63
.....E.EKVKN.....GR.....E..NG.SQNSN---S---E-----ID..RDYKKEEQ.A-----T.....	PAK
.....KA.EK---E..HYTSPV.....K.N---D...R-----I..N...L..N.Y-----Y.S.....Y.	SB12
.....QD...K---E..RHTNPV.....NA.....R-----I...HSSNGKL-----	SB29
R-----K.D.E--N..T..G.Y.....L.....IQ....R.LPK-----S.....Y.	SB30
.....M.KD.E--N....KDTP.....RAP.SN.NHQN...Q-----I..R.INLP-----S.....Y.	SB32
GEPNSFSEDE--L..KRG-----SSE--E.KW.DG-----QSRVVGTYTNFT..R..YV.LNK--NNI.I..NIV--LFGPDG..Y.K.KEPS	B16B6
TKPKELPKRQK.V...VETDGDSDIYSSPY.TR.NHQNGSAGNGVN---QPKNQATGHENFQ.....WF.KHAA.EK.FS.K.I--KSGDDG.IF.H.EKPS	M982
TEPKKLPLKQQ.V.SEVETNGNSKMYTSPY.SQDA.SSH--ANGAN---QPKNEVTDYKKFK.....WF.KHAK.EVKNE.GLVSAKRGGDG.IF.H.DKPS	FA19
-----D..VITNGNL.DVPYK.NSSKYNYPDI.....KTKDSSLQ..R..YVIDGEH.GSNE-----VY.	AP205
-----VELSED.IT.LYQESVEIIPH.DELNGKTTSDNVYHS---DSKRLDKNRDLK..R..YV.DG.FNEIRNRDNG.HVFKQGID-----VY.	AP37

FIG.15B.

YGNKTATNLPVNGVAKYKGTWDFITATKNGKRYPLLSNGS---HAYYRRAIPEDIDLENDSKNGDI-GLISEFSADFGTKKLTGQLSYTKRKT-----N  
 F.T.SA...G...T...S...AE...N.E.R.SGGG-Q.S...T...DRKT-----T...TVN...G.Y.NL.E.DAN-----K  
 E.K...K...N...E...S.F.SIG--Q.S...S...YNLENGDA-----V...K.E...E.Y.NE...SVN-----E  
 F.KQ...T...KVT...S...AE...S...F...Q...F...VKNDENREK.V...G.F...Q...-----H  
 S.I...S...Q...S.FGSF--G.N...S...NLENNLKNGA-.T...TVN...K.Y.NE.E.-----N  
 F.K.E...T...E.T...R...S.S...NR--Q.SK...ETR-.T...TVN...G.Y.HL...NAN-----E  
 F.KQ...T...E.T...S...ER.N.S.FN.RG--Q.S...T.G...A-.T...TVN...EPY.NE.E.N-----L  
 KLP-SEKITVK.TWD.VTDAMEKQRFEG-L-GSAAGGFKSGALSALFEGVLRNQAAS--SGHT.F-.MT...EV.SD.TIK.T.YRNN.I.QNNSENKQ  
 RQLPASGKVIYK..WHFVTDTKKGQDFREIIPQSKQGDYSGFGSGDSEYSNKNESTLKDDHEGY-.FT.NLEV..N...K.IRNNASLNNNTNNDK  
 RQLPASEAVIYK..WHFVTDTKQGQKFNDILETSKGQGDYSGFGSGDDEGETSNRT.SNLND.HEGY-.FT.N.KV..NN...K.IRNNKVINTAASDG-  
 K.SP.KE...QLLT.T.S...TSNANLNNEEGRPNYLN--DD..TKFIGRVLVSG.A.PAKH-KYT.Q.EV.A..M..KJ.-D.E..-----  
 L.VTPSKE..KGK.IS.....VSNINLEREIDGKDTSGDGKNVSATSITETVNR.HKVGE.L..N-EVKGVASSEFAVDFDNKKLTGSLYRNGYINRNK  
 AP37

NQ--PYEKKKLYDIDADIYSNFRGTVKPTKED-SEEHPTSEGT-LEGGFYGPNAEELGCKFLATNDRVFGVFSAKETEETKKEA-LSKETLIDGLITFFS  
 S.--NRTH-...LE.VH...K...K.ES...EGQ...H.KK.L...Q.Q..SENKK.P...T...K  
 S.--NTTH-...TLE.KV...K...KTK-.D...N.EK...DPQNPENQK.T...K  
 I.--NH...H...K.N.Q.-K...EGQ...G.KK...G.N...P...T...  
 NKLOKR.HE...K...TQKD.Q...G...DKK-.R...K  
 --NR.H...NLE.V...KES-...S.KK...Q.Q..EENKK.L...T...  
 --SKDR.H...LE.V...K.ES...S.KK...KP...P...T...  
 IK--TTRYTIQATLHGNRFKGAALAD,GATNG-...I.DSDS...KG...A...SN..K.AA.G.QKDKKDG.NAAGPA.E-----  
 HT--TQYYSLDAQ.TGNRFNGTATA.D.KENET-KL-...V.DSSS.S...F.QG...FR.SD.QK.AV.G...TKDKLENG.AA.GS.GAAASGGAAG  
 YT--TEYYSLDATLRNRF.GKAIA.D..NTGGTKL-...VFDSSS.S...F.QG...FR.SD.GK.AV.G...TKDSTANGNAPAASSG-----  
 IY--TV---NA..RGNRFTGAATASD.NKG.GE.YNF-.SADSQS...K..MA..V.N.KSL.A...-----  
 A.----VT.R.S.E...AG...KA.A...AGD---IFTDSNY...K...MA...FTNNKSL.A..A...-----  
 EAGAN  
 DL63  
 PAK  
 SB12  
 SB29  
 SB30  
 SB32  
 B16B6  
 M982  
 FA19  
 AP205  
 AP37

TKKTDAKT---NATTSTAANTTTDTTANTITDEKNFKTEDISSFGEADYLLIDKY-----PIPLLPDKNTNDFI  
 .TNAT.NATT--D...T.S.K...T.ATANTE..T.K.P.L...N...V..F.--ESG...  
 RTDATTNATT--D.K.ATTD.A.S...KK.AE...GNQ-----E...D...  
 .T...NATA...AE...K...N...V...-ESG...  
 EAGAN  
 DL63  
 PAK  
 SB12



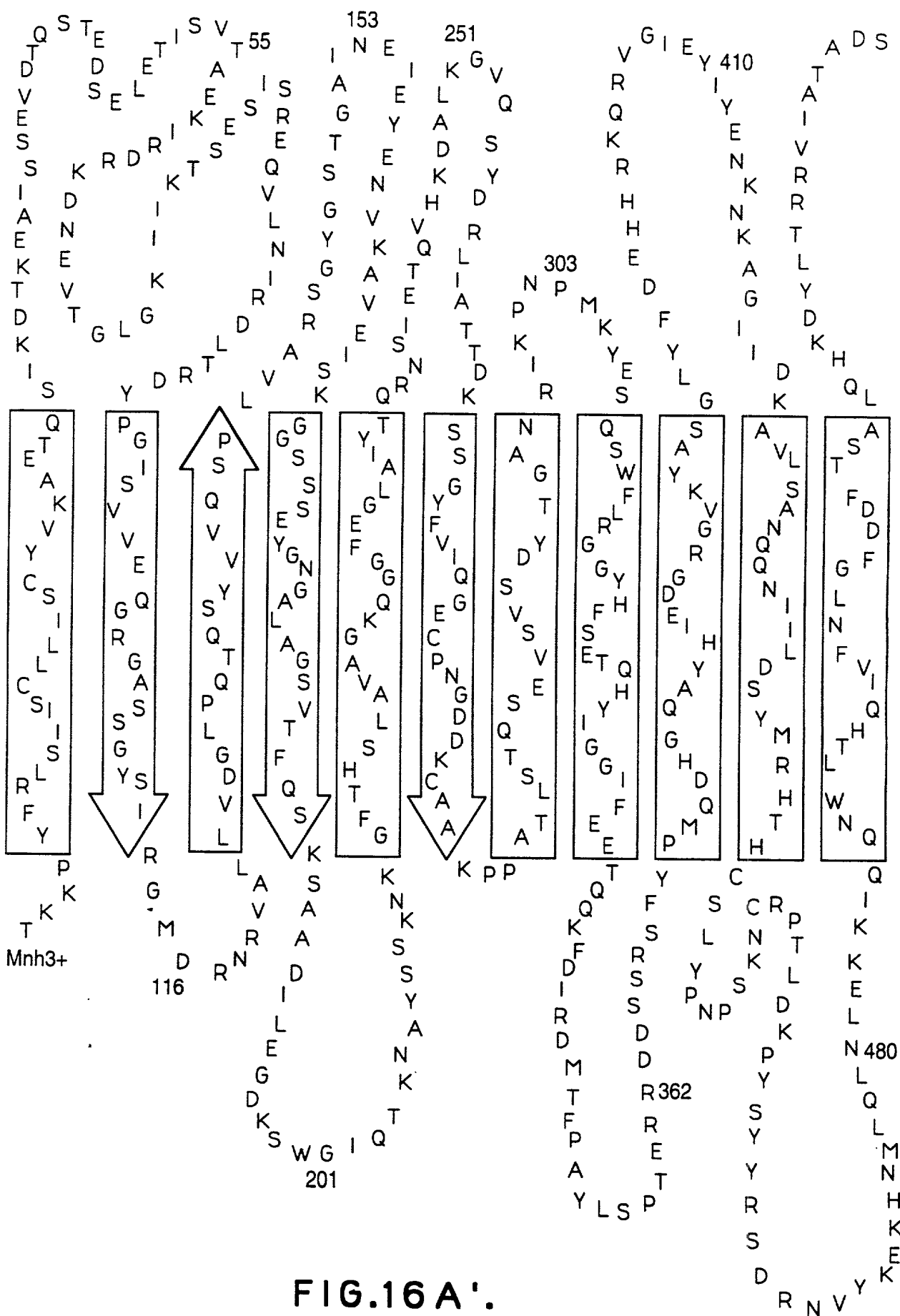
## FIG.15C.

.....T-----A.AK.....T.K.P.....N-----V..F.EE.....	SB29
.....N.T-----D.....S.ATNATA,AE..T.K.....N-----V....-E.....	SB30
-----KTTD...NK.TSAK.NTE..T.K.P.....N-----.....-ESG.....	SB32
-----VID.YRI.GEEFKQEIDSGFVKLLVD.VELS..PSEGNKAA-----FQHEIE-----	B16B6
.S-----SENS--KL..VLD.VEL.LNDKKIKLNDNFSNAAQLVVD.IMIP..PKDSESGNTQADKGKNGGTEFTRKFEHTPESDKKDAQAGTQTNGAQTASN	M982
PGAATMPSET--RL..VLD.VEL.PDGKEIKLNDNFSNATRLVVD.IMIP..PT--ESGNGQADKGKNGGTDFTYETTYTPESDKKDTKAQTGAGGMQTASG	FA19
-----HNGSNVN.VRIIDASKI.LT..SISELNN..D.SV.I..-----GKKIKLAGSG.T	AP205
-----SENG--ET..E-----RIIDA.KI.LTQ.NAKELNN..D.SV.I..-----GQKI.LAGVN.K	AP37
SSKHHTVGNKR--YKVEACCSNLSYVKFGMYIEDPLKEKETETETETETEKDEKEKDEKDEKQTAATNTYYQFLLGHRTPKDDIPK--TGSAKYHGSWFG	EAGAN
.....K.T--Q.....A.P.--E.K.K.KD.....ATTSIK.....L...SSE.....-E.....N....	DL63
.....G.T--.....K.....KDKDN.NETDKEKGKPT.TTSI.....L....E....-E.....N....	PAK
.....K.T--Q.K.....V.P.E.....--KE.E...ATNLS.....L...SSE.....-G.....L....	SB12
T.R..K..D.T--K.....K.....NG.NG.....E.....ATTSIK.....A.A...A--NV..R.N....	SB29
.....E.G.H--K.....I.....--N.N.KIE.EQ.H...L...SSQ..A--NV..R.....	SB30
.....E.G.--K.C.....KENNKN.T.E.....TTSIK.....L...SSE.....-M.NVT.R.....	SB32
-----QNGVKAT-----V.....D.MS..KLSKEN-----DDM..Q.V...VS.VAARTEAN...R.T.Y.	B16B6
TAGDTNGKT.T--E.V.....N.L.Y..LTRKNS-----SAMAQAGNSSQADAKTEQVEQSM..Q.E..DEKE...--TDQNVV.R...Y.	M982
TAGVNGGQVGTKT...QV.....N.L.Y.LLTREN-----NNSVMQAVKNSS.AD.K.KQIE.SMFLOGERT.ENKIPQEQGIV.L.F.Y.	FA19
NKHTIEING.T--MVAV.....E.M...QLW-----QQAEGGKPENNSL..Q.E..AT.KM...--G.NY..I.T.D-	AP205
N...TVEING.T--MVAV.....E.M...QLW-----Q.EGKQVVKDNSL..Q.E..AT.KM.A--G.NY..V.T.D-	AP37
YITDGKTSYSPSGDKKRDKNVAEENFVDFAEKKLTGELKRHDTG-NPVFSIEANFNSSNAFTGTATATN--FVIDGKNQKNTPINITTKVNGAFYCPKA	EAGAN
...S.E...A...E.S.....N.....T.....Q-...K.N.T.QSGK.D.....KD--LA....T.GTSKVNFTA.-.....	DL63
...S.E...A...E.S.....D.S.N.T.....N.-T.K.N.EL.G.-.D.....N....TS.AK.....	PAK
LS..S.....EN..L.....N.VD.T.KGQ.I...NQ-T..T.D.T.KGK.N.....N.--VA..POSTQGTSNVNFTA.-.....N.	SB12
...G.D...TT-----D.N.D.T..T.....N.-...T.N.S.QSGK.D.....N.--VA..PQ.T.TTTSRVNFTA.-.....	SB29
...G.D...TT-----L..D.N.TD.....A.NQ-T..R.N.D.K.ND..K.....E.--N....TG..Q..K.E.....N.	SB30
...G.D...AT...RQ...P...A..NN.....TS.....NQ-...N.K.T.Q.GR.D.E.....E.--D..G-	SB32

FIG.15D.

..AN.-..W.GEASQEGG.-R...D...ST...IS.T.TAK.RT-S.A.T.T.MIKD--.G.S.V.KTGENG.AL.PQ.TG.SHYTHI-EAT.S.G....KN.	B16B6
H.AN.-..W.GNASD.EGG.-R...T.N..D..I..K.TAENRQ-AQT.T..GMIQG--.G.E...KTAESG.DL.Q..TTRTPKAYITDA..K.G.....	M982
R.AN.-..W.GKASNAT.G.-R.K.T.N.DR.EI..T.TAENRS-EAT.T.D.MIEG--.G.K...KMG.DG.AP.QN..TVTHKVVHIANAE.Q.G....N.	FA19
AQVSKENNWATA.DD.KSGYRT..D...GN.N.S.K.LFDKN.V...TVD.KIDG--.G...K.KTSDEG.AL.SGS.RVE.VKF.DVA-.S.G....T.	AP205
ALVSKG.NWIAEA.NN.ESGYRT..D.N.SD..VN.K.-FDKG.V...TVD.TI.G--.G.I.S.KTSDSG.AL.AGS..HG.AVFSDI-...G....T.	AP37

SELGGYFTYNGN-STATNSESSSTVSSSSNKNARA-AVFGAR-QQVETT-K*	EAGAN
T.....-NPTDKN.....EK.....KK.....*	DL63
.....KNP.....P.PP..P..S.....KK.....N.*	PAK
T.....-PTDK.....P.....-.....*	SB12
T.....-NPTDKN.....P.-.A.....KK.....N.*	SB29
T.....KNP.DK.....P.PP..P.....KK-...KNN.*	SB30
.....KDTTK.T.....P.PP..P.....KK.....N.*	SB32
I.M..S.SFP..APEGKQE-----K.S.....KR..LVQ*	B16B6
E....W.A.P.DKQ.EKAT----AT..DGNSASS.T....KR..PVQ*	M982
E....W.A.P..EQ.KNA-----E.GNGNSASS.T....KR.KLVK*	FA19
A....Q.HHKSENGSVGA-----K-...KK*	AP205
G....Q.HHKSDNGSVGA-----K-R.I.K*	AP37



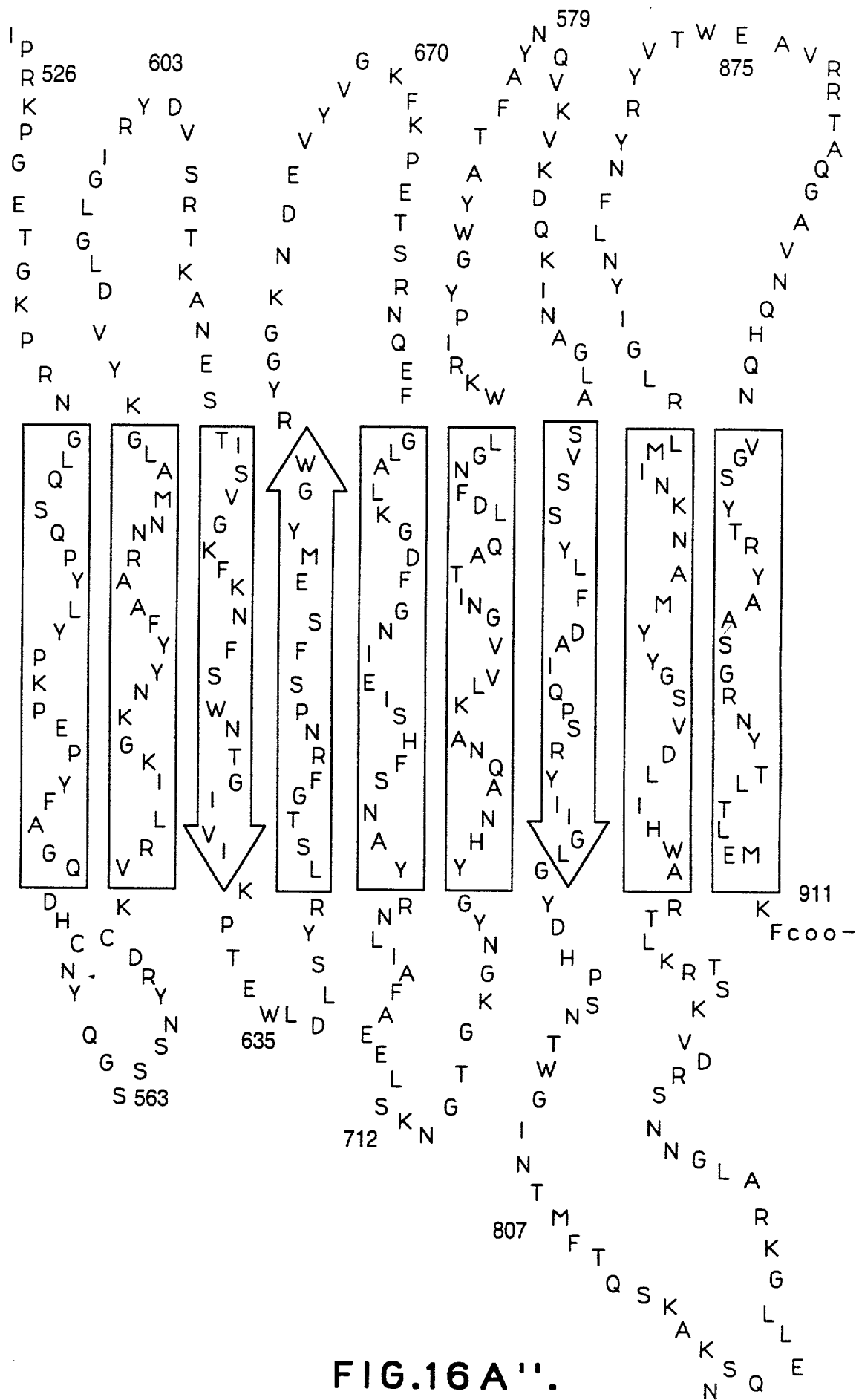


FIG.16A''.

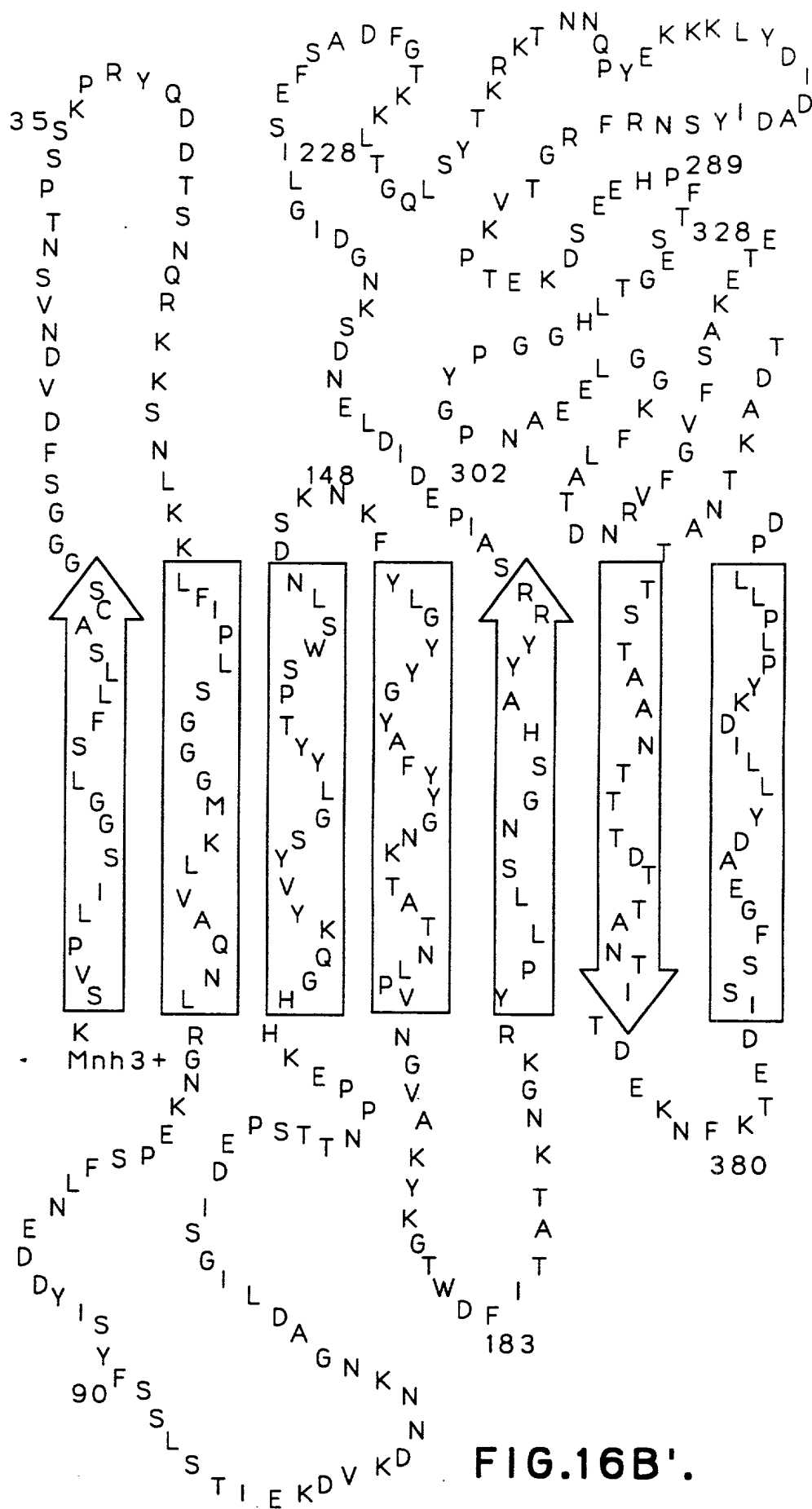


FIG.16B'.

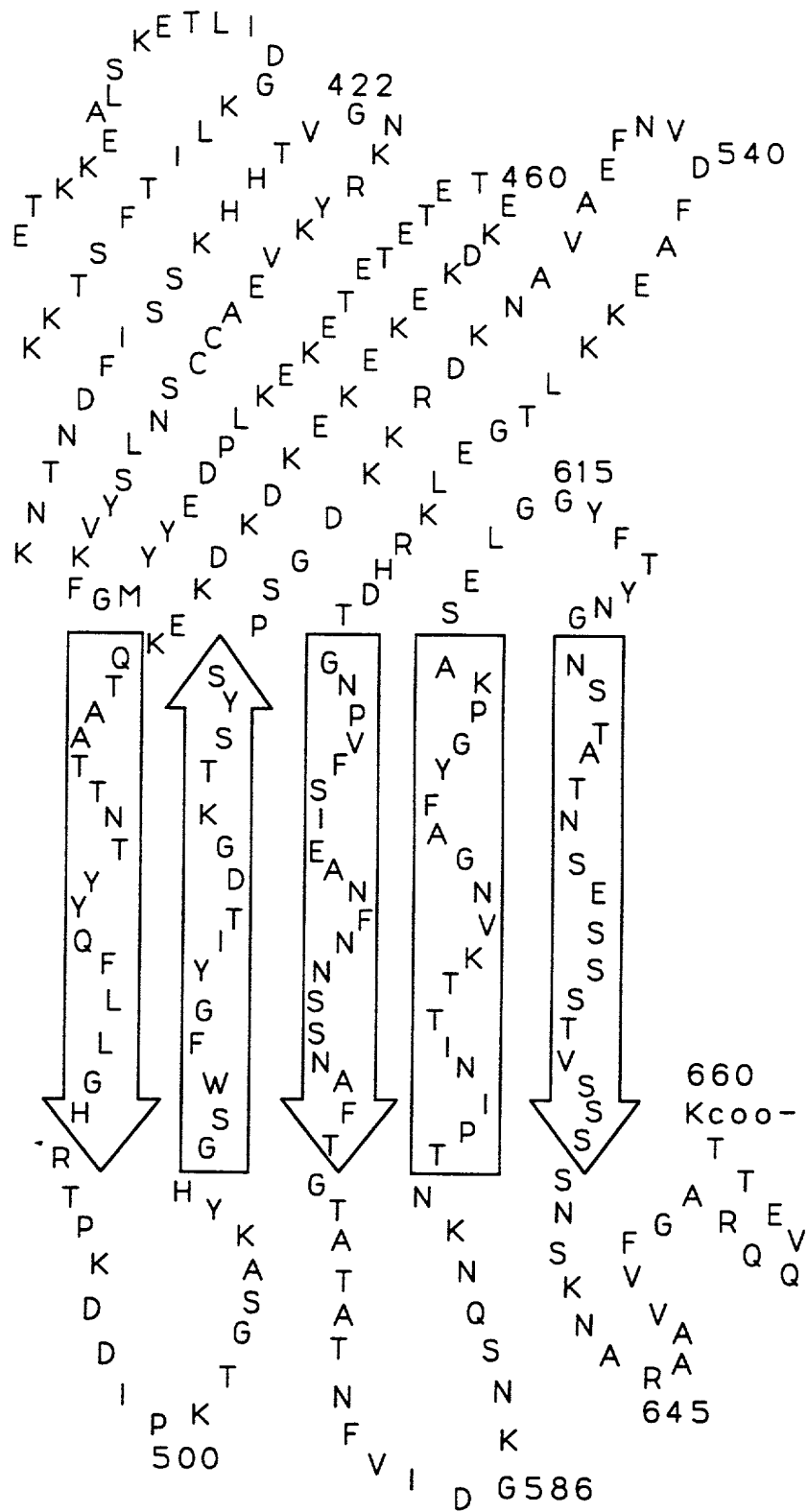


FIG.16B''.

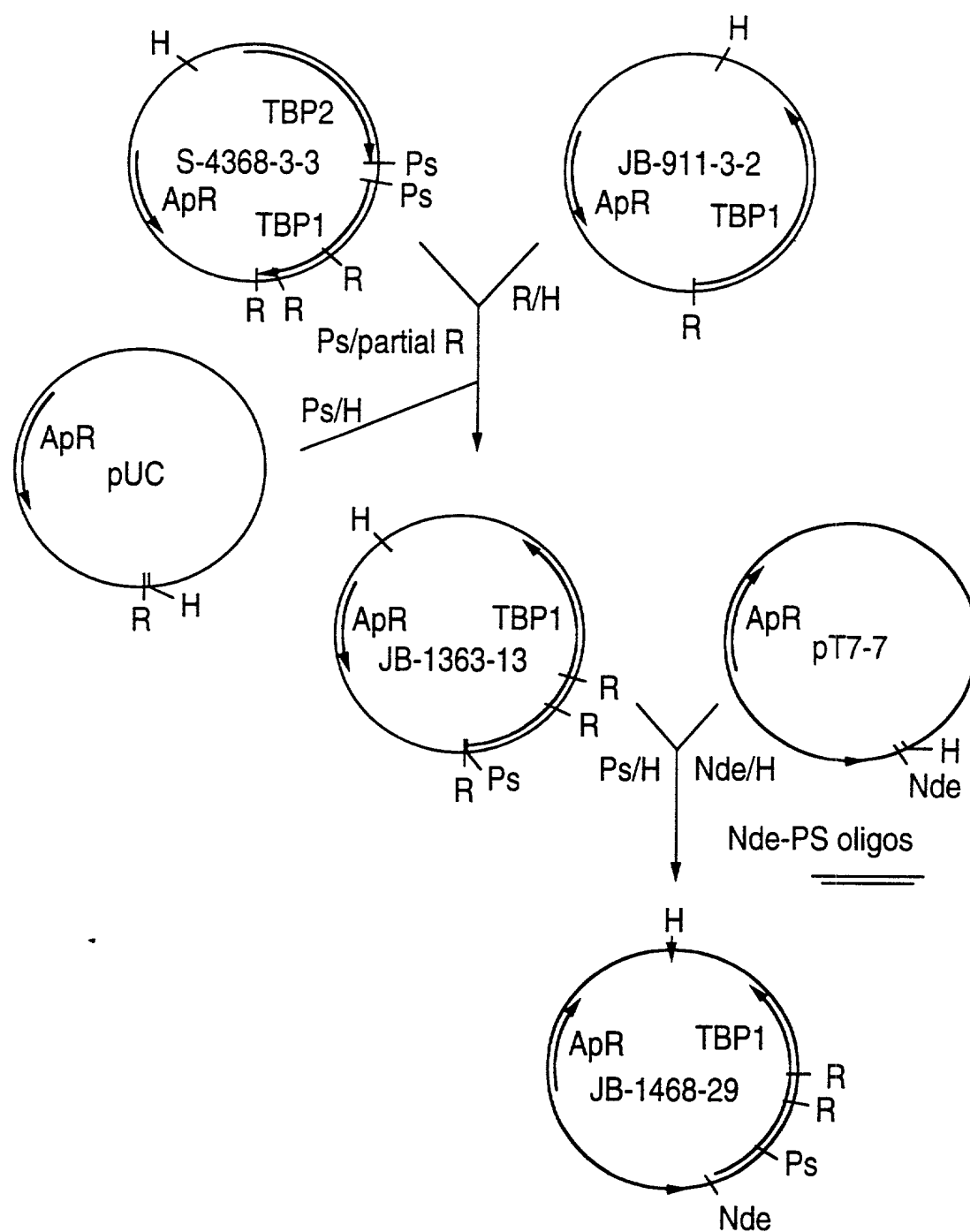
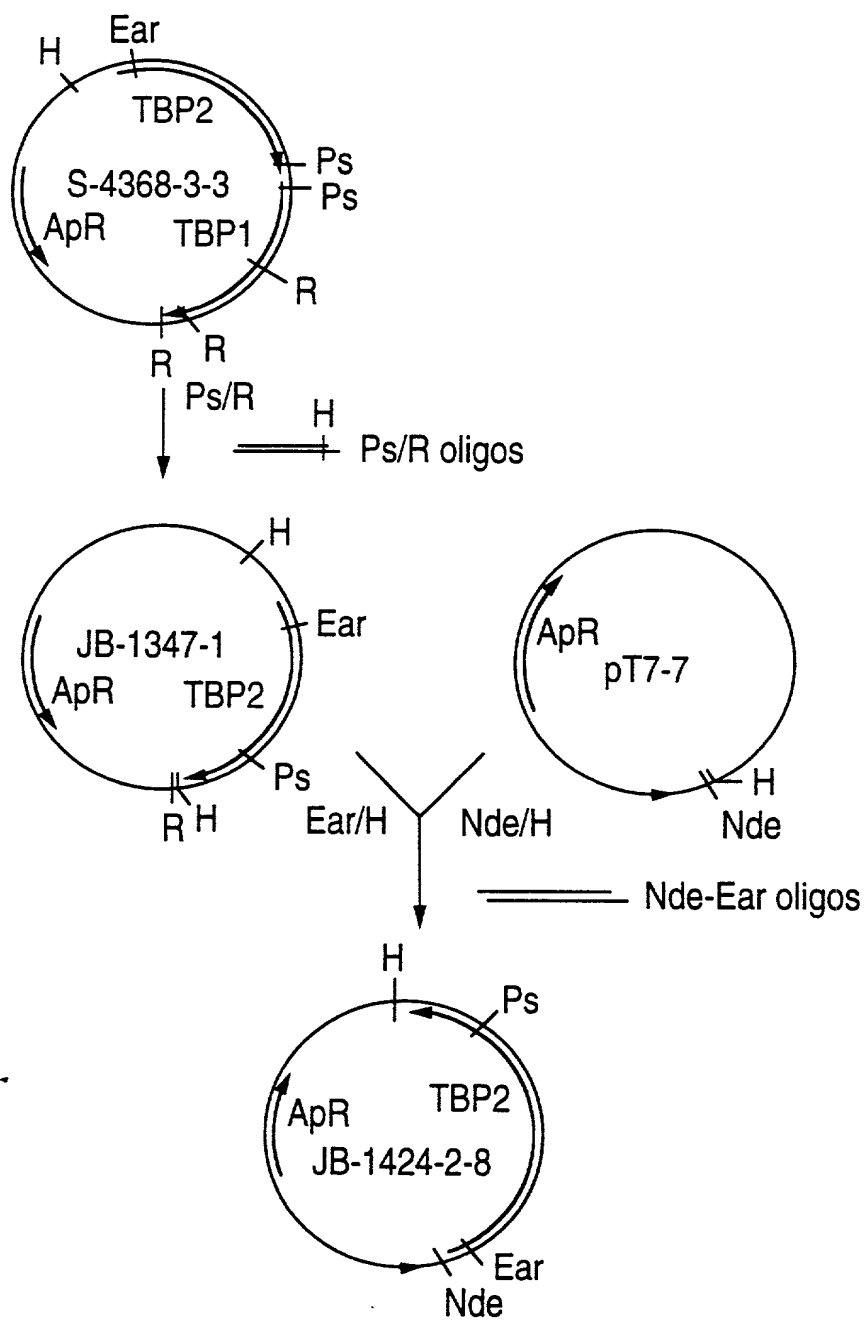


FIG.17.



**FIG.18**



**FIG.19.** Oligonucleotides to express TBP2 with no signal sequence.

Nde I

# Far I

TATGTGTTCTGTGGTGTCTTTTCGACGTTGACAACGTTTCTAACACTCCCTCTTCT  
ACACAAGACCACCAAGAAAGCTGCAACTGTTGCAAGATTGTGAGGGAGAAGATT

ATG start codon is underlined

TGT cysteinr of mature protein is double underlined

## FIG.20A.

Sequence of oligonucleotide pairs (A, B, C and D) for constructing TBP1 and TBP2 expression plasmids

Oligonucleotide pair A (Seq. ID 86 and 87) to join the T7 promoter and Egan TBP1 gene

Nde I

TATGGAAACTCAAAGTATAAAAGATACAAAAGAGCTATATCATCTGAAGT...  
ACCTTTGAGTTTCATATTTTCTATGTTTTTCTTCGATATAGTAGACTTCA...

Pst I

...GGACACTCAAAGTACAGAAGATTTCAGAATTAGAAACTATCTCAGTCACTGCA  
...CCTGTGAGTTTCATGCTCTTCTAAGTCTTAAATCTTTGATAGAGTCAGTG

Oligonucleotide pair B (Seq. ID 88 and 89) to join the T7 promoter and Egan TBP2 genes through the *E. coli* lpp leader

Nde I

TATGAAAGCTACTAAAGTGGTTCTGGGTGCTGTTATCCTGGGTTCCACTCTG...  
ACTTTCGATGATTTGACCAAGAGACCCACGACACATAGGACCCCAAGGTGAGAC...

Ear I

...CTGGCTGGTTGTAGCGGAGGTGGTTGTTTGTATGTAGATAACGTCTCTAATACCCCTCTTCT  
...GACCCACCAACATCGCCTCCACCAACAAAACATACATCTATTGCAGAGATTATGGGGGAGAAGATT

## FIG.20B.

Oligonucleotide pair C (Seq. ID 90 and 91) to join the T7 promoter and Egan TBP2 genes through the *E. coli* rlp B leader

Nde I

TATGCGATATCTGGCAACATTGTTGTTATCTCTGGCGGTGTTAATCACCGCTG...  
ACGCTATAGACCGTTGTAAACAACATAGAGACCGCCACAAATTAGTGGCGAC...

Ear I

...GTTGTAGCGGAGGTGTTCTTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT  
...CAACATCGCCTCCACCAGAAGAACTACATCTATTGCAGAGATTATGGGGGAGAAGATTT

Oligonucleotide pair D (Seq. ID 92 and 93) to join the T7 promoter and Egan TBP2 genes through the *E. coli* pal leader

Nde I

TATGCAACTGAACAAAGTGCTGAAAGGGCTGATGATTGCTCTGCCCTGTTATGGCAA...  
ACGTTGACTTGTTTCACGACTTTCCTCGACTACTAACGAGACGGACAATACCGTT...

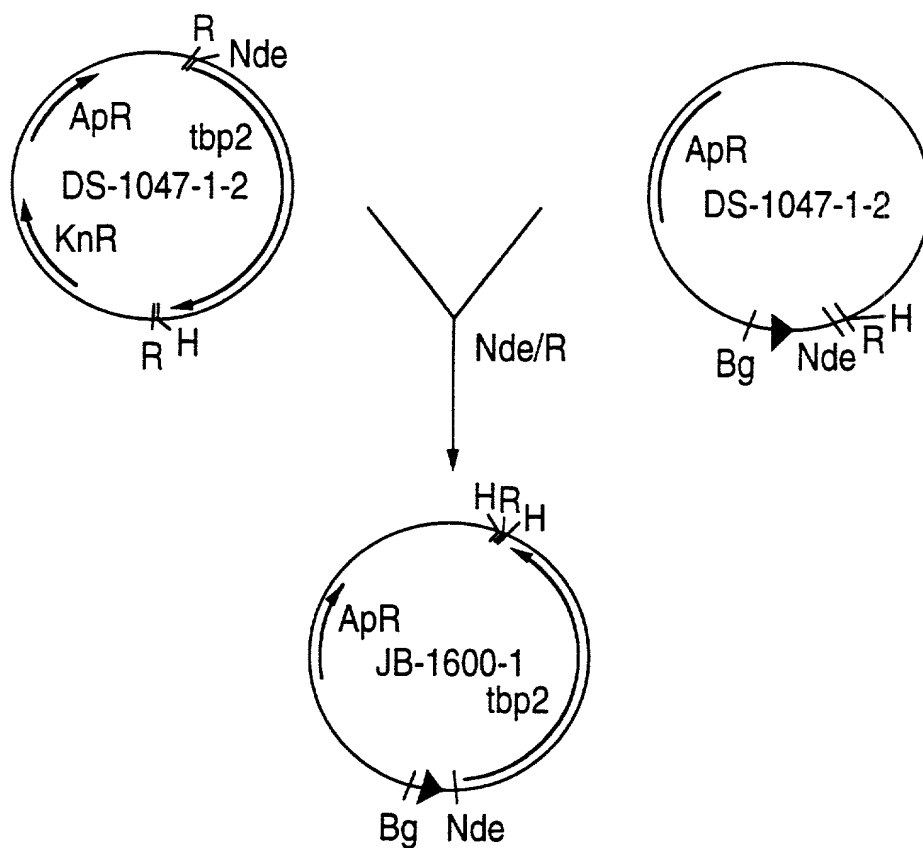
Ear I

...TTGCTGTTCTAGCGGAGGTGGTTCTTTGATGTAGATAACGTCTCTAATACCCCTCTTCT  
... AACGACCAACATCGCCTCCTACCAAGAAACTACATCTATTGCAGAGATTATGGGGGAGAAGATTT

ATG start codons are underlined

TGT coding for Cys of lipoproteins are double underlined

TGT may be replaced by TCC coding for Ser to secrete non-lipoprotein



**FIG.21.**

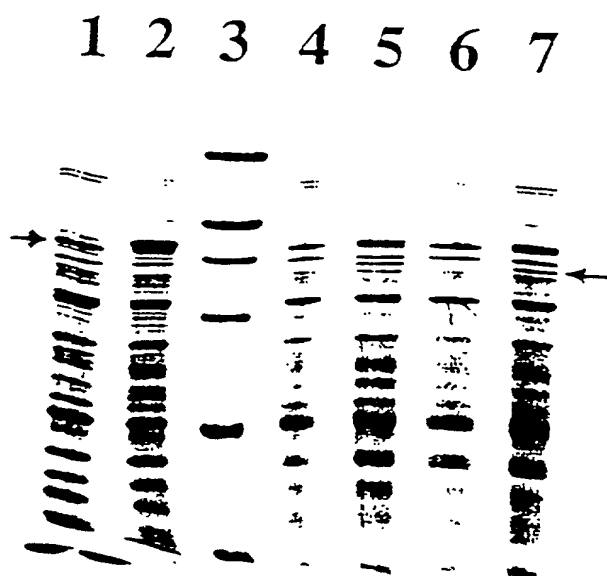


FIG.22.

## PURIFICATION OF rTBP1/ rTBP2 FROM *E. COLI*

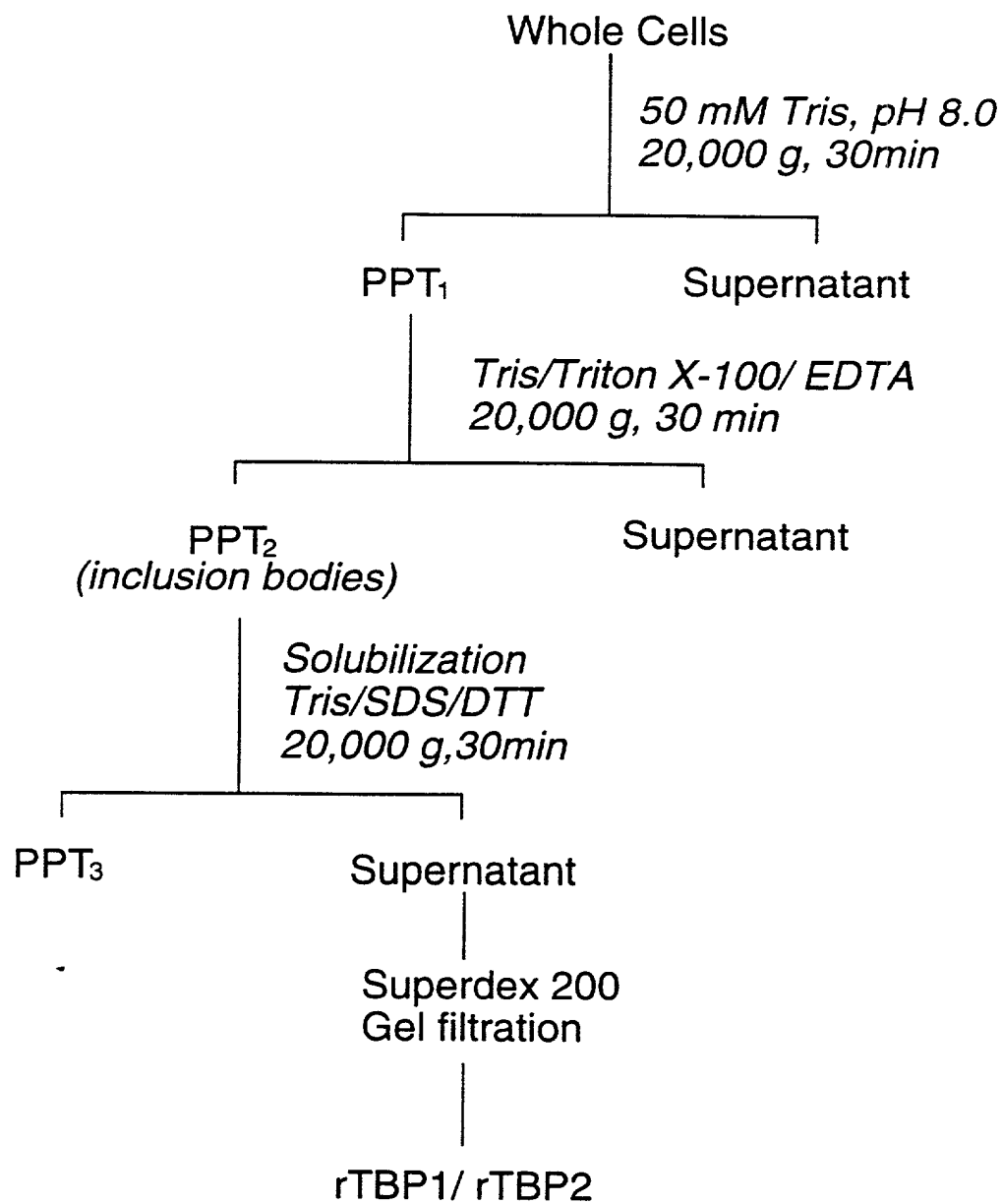


FIG.23.

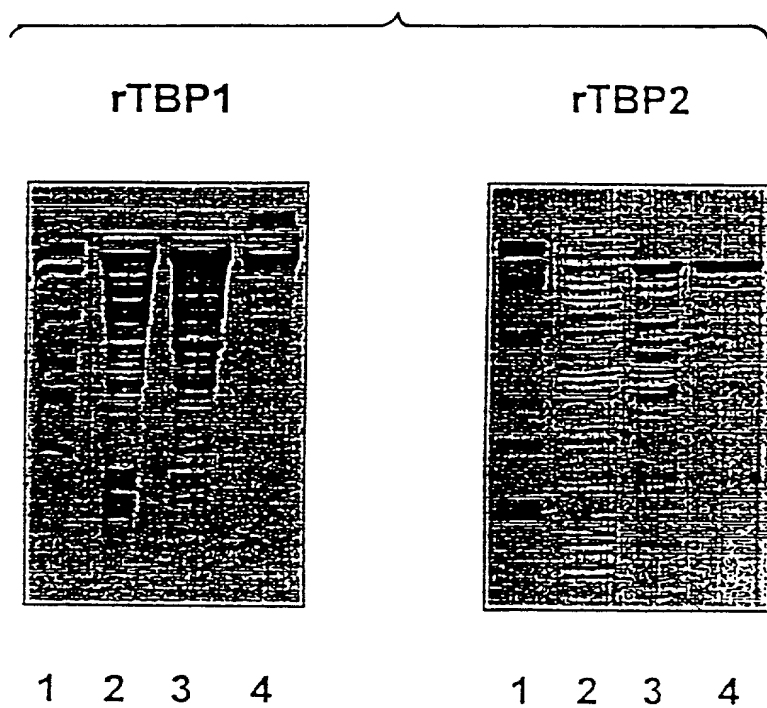
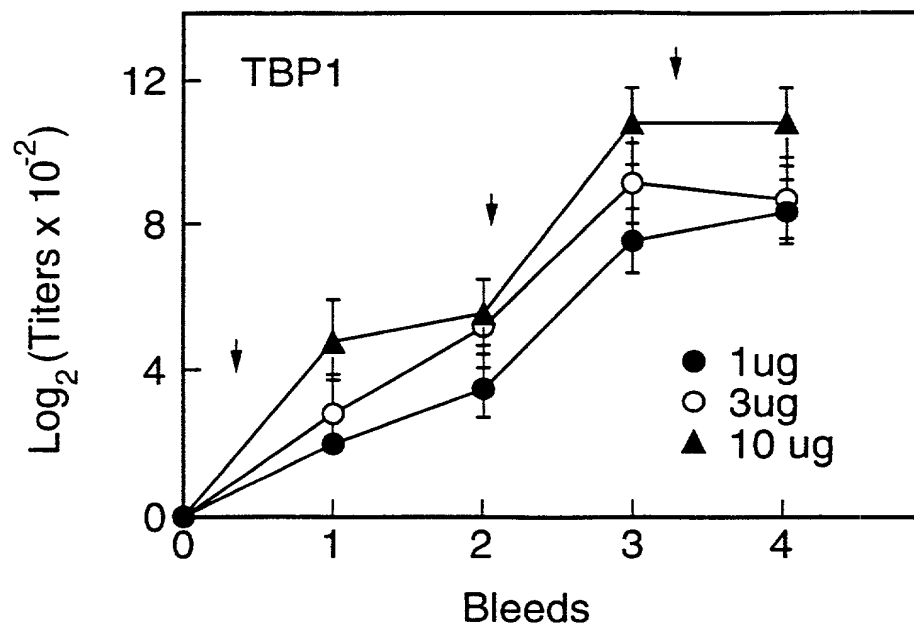
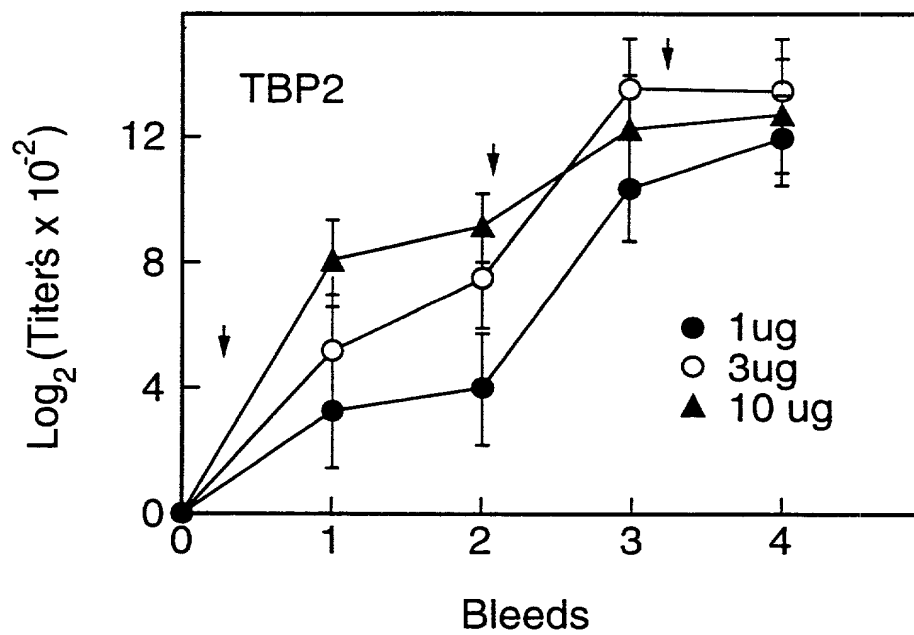


FIG 24

## Kinetics of Antibody Response to TBP1/TBP2 in Mice



**FIG.25 A.**



**FIG.25B.**



1 2 3 4 5 6 7 8 9 10 11 12 13 14 15

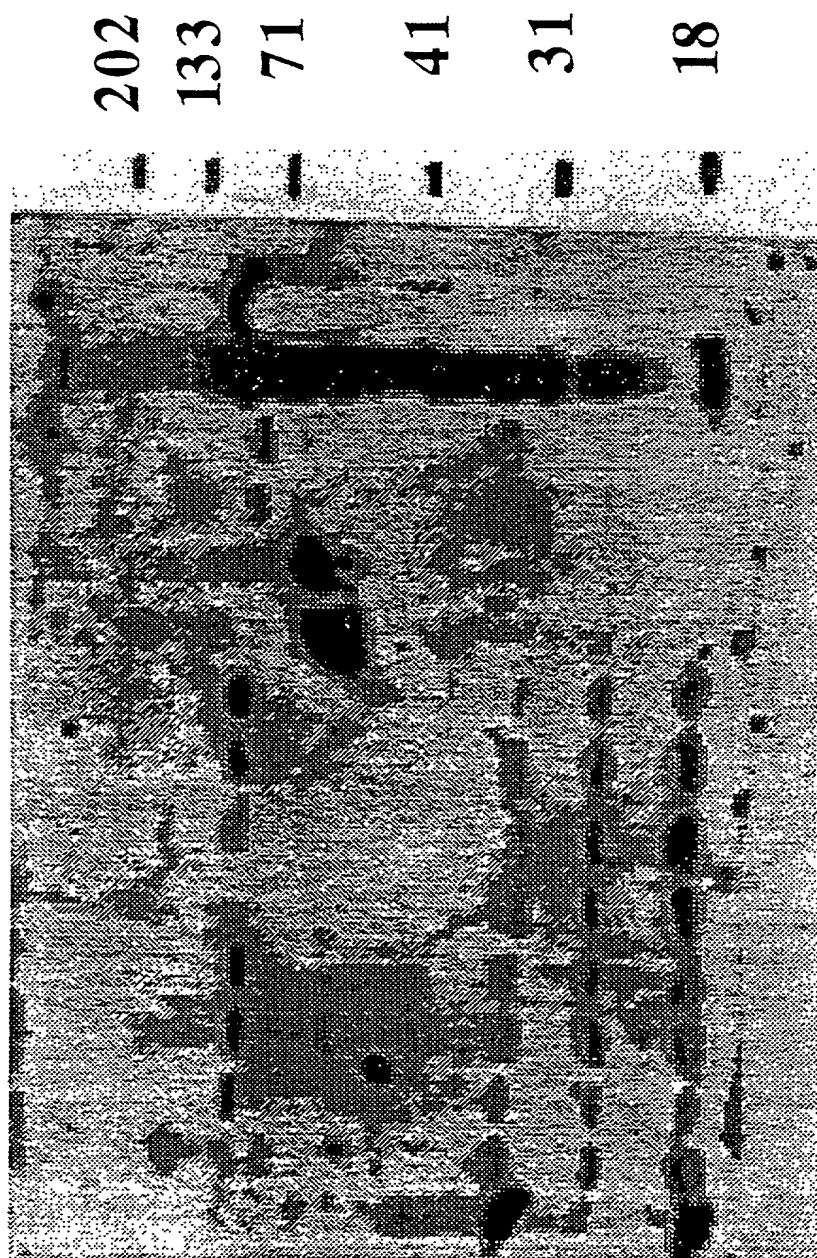


FIG.26.

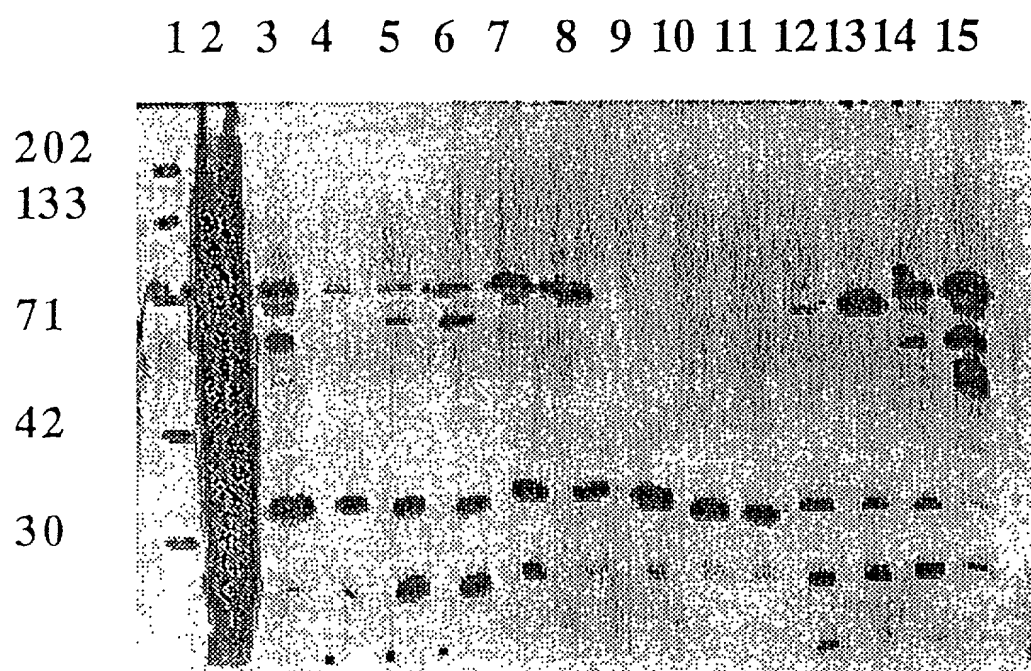


FIG. 27.

# Construction of plasmids pUHIT1KFH and pUHIT1KFP

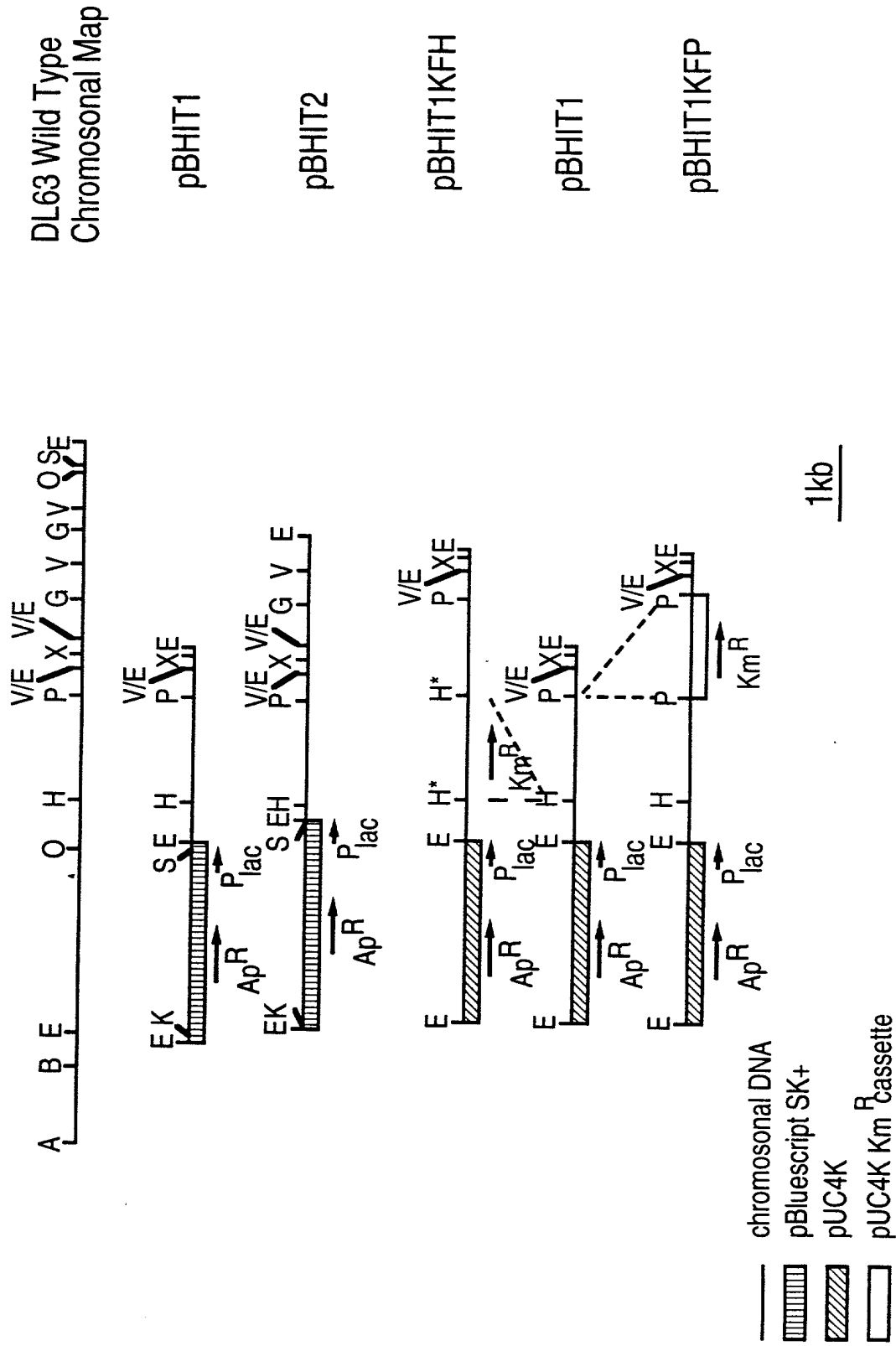
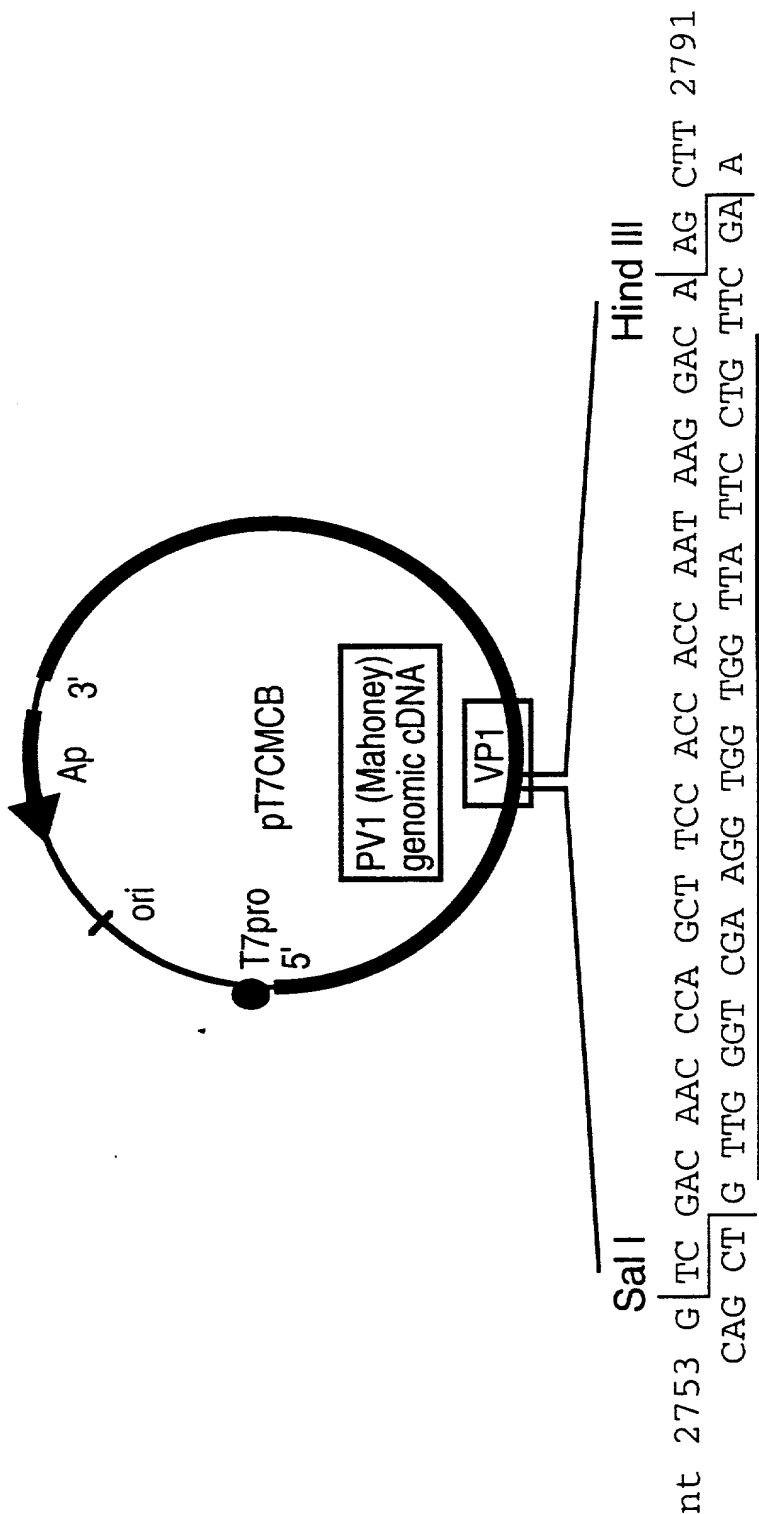


FIG.28.



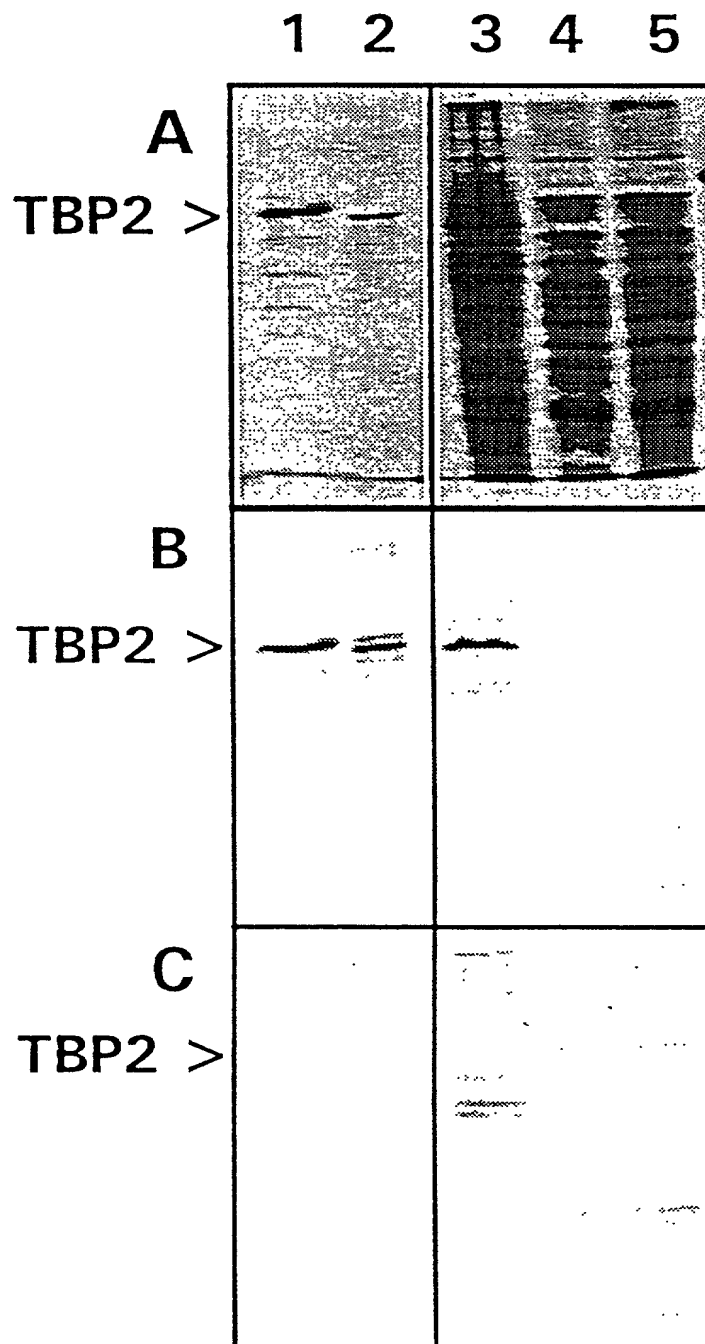
aa1094 V D N P A S T T N K D K L 1102

Clone	Sequence encoded	SEQ.	Viable virus
		ID NO:	recovered/ strain designation

pT7XLD	NPASTTNKD	132	Yes/PV1-XLD
pT7TBP2A	NPASTTSLEGGFYGPKD	133	Yes/PV1TBP2A
pT7TBP2B	NPASTTSLEGGFYGKD	134	Yes/PV1TBP2B
pT7TBP2C	NPASTTLEGGFYGPKD	135	Yes/PV1TBP2C
pT7TBP2D	NPASTTLEGGFYGKD	136	Yes/PV1TBP2B

FIG.29.

FIG.30.

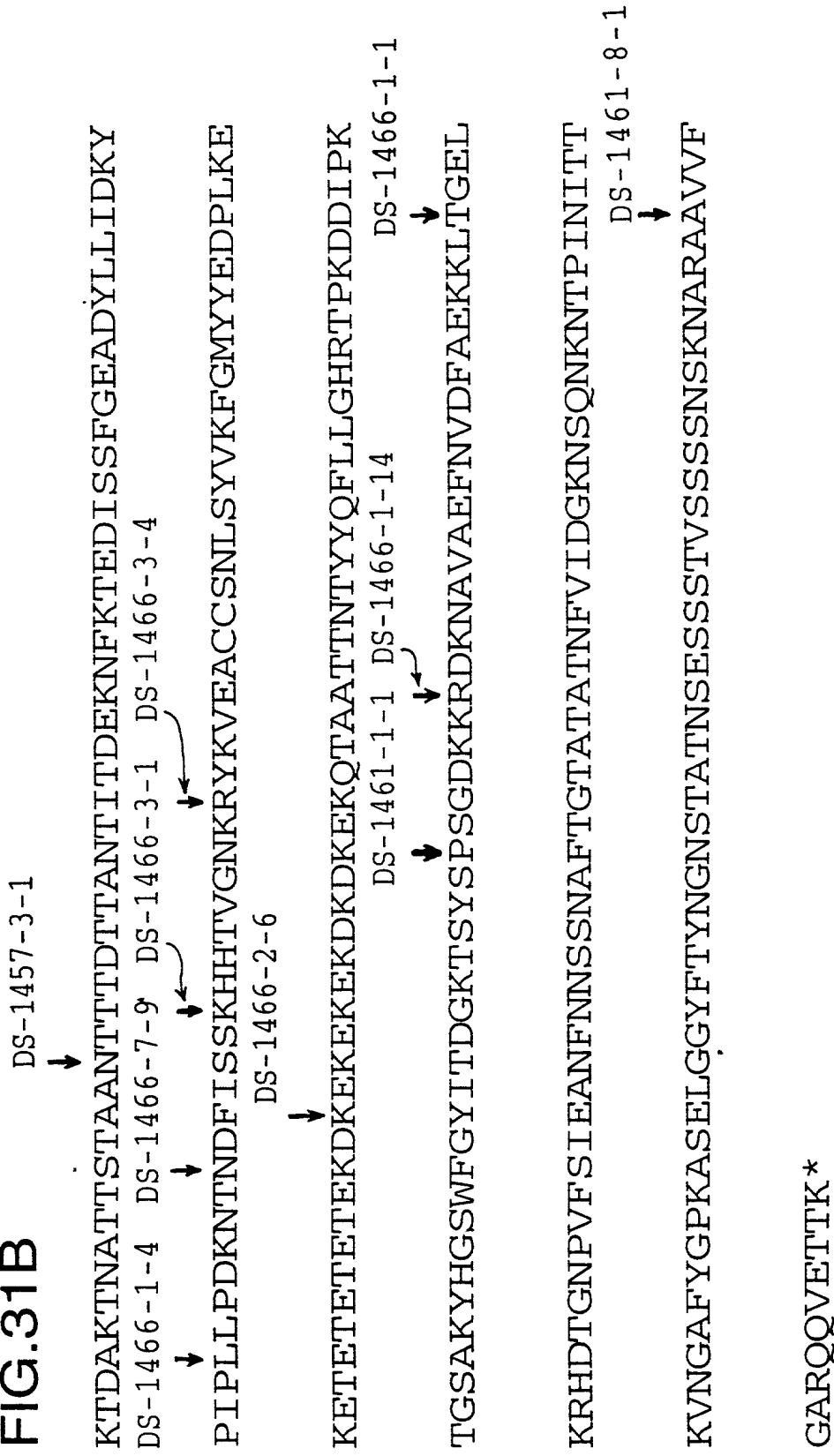


## FIG.31A

Eagan Tbp2

MKSVPLISGGLSFLLSACS<sup>↓</sup>GGGFVDNVSNTPSSKPRYQDDT'SNQRRKS  
 Signal Sequence DS-1466-1-18  
 NLKKLFIPSLGGMKLVAQNLRGNKEPSFLNEDDYISYFSSLSTIEKDVK  
 DS-1466-4-3  
 DNNKNGADLIGSIDEPTTNPPEKHHGQKYVYSGLYYTPSWSLNDSKNKF  
 YLGYYGYAFYYGNKTA<sup>↓</sup>TNLPVNGVAKYKGTWDFITATKNGKRYPLL'SNGS  
 HAYYRRSAIPEDIDLENDKNGDIGLISEFSADFGTKKLTGQLSYTKRKT  
 DS-1466-5-1  
 NNQPYEKKKLYDIDADIYSNRFRGT<sup>↓</sup>VKPTTEKDSEEH<sup>↓</sup>PFTSEGTLEGGFYG  
 DS-1466-4-1  
 PNAEELGGKFLATDNRVFGVFSAKETEETKKEALSKETLIDGKLITFSTK

FIG.31B



Molecular Weight ( $\times 10^{-3}$ )

### SDS-PAGE

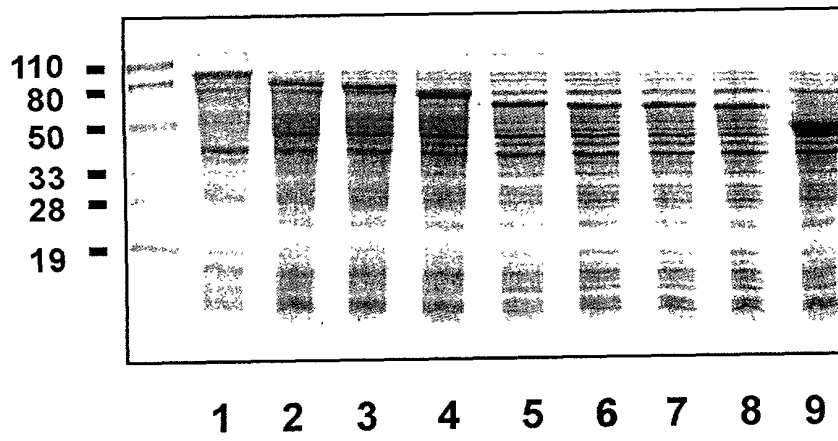


FIG 32 A.

### HTf- Binding

Molecular Weight ( $\times 10^{-3}$ )

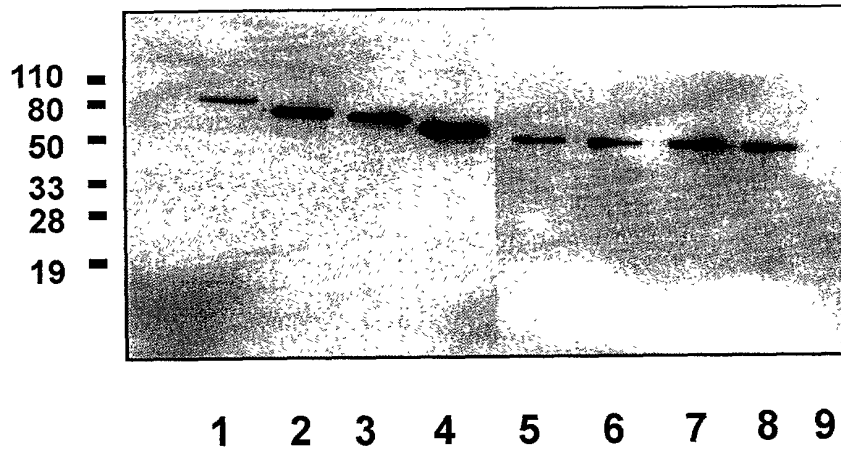


FIG 32 B.